Mycobacte Mycobacte Mycobacte Mycobacte Mycobacte Antigenic rcobacte

Mycobacte Mycobacte Mycobacte Mycobacte

Ra12-H9-3

Mycobacte Mycobacte Antigenic Mycobacte

cobacte

Run

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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TbRa35. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen,
                                                                                                                                                      Aaw32354 Mycobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection.
                                                                                                                                                                                                                                                                                     Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
                                             Aae17574 |
Aau74599 |
Aae29708 |
Aae29772 |
Aae29731 |
Adae29731 |
Adae29731 |
                                                                                                                     Aae17573 | Ada26374 | Aau74588 | Aay32059 |
                                                                                                                                                                                                                                                                                                                                                                                                                                               Houghton R;
                             Aay32070
                                     Aae29710
                                                                                                                                                                                                                                                                                                                                                                                                                                                Campos-Neto A,
                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis antigen TbRa35
                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 124-126; 190pp; English.
                                                                                                                              ADA26374
AAU74588
AAY32059
                                               AAE17574
AAU74599
AAO22142
                                                                                                      ADA26364
AAE29709
AAE17573
                                                                      AAE29708
AAE17572
ADA26373
AAE29731
                                                                                                                                                       AAW32354
                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC,
DR;
                                                                                                                                                                                                                      AAW32367 standard; protein; 355 AA
                                                                                                                                                                                                                                                                                                                                                                               95US-00523435.
95US-00532136.
96US-00620280.
96US-00658800.
96US-00680573.
                                                                                                                                                                                                                                                                                                                                                                 96WO-US014675.
                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
                                                                                                                                                                                                                                                         (first entry)
Reed SG, Skeiky YAW,
Vedvick TH, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-192904/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT91414
 WO9709429-A2
                                                                                                                                                                                                                                                                                                                                                                 30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-1995;
22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1995;
                                                                                                                                                                                                                                                         13-JAN-1998
                                                                                                                                                                                                                                                                                                                                                 13-MAR-1997.
 AAW32367;
                                                                                                                                                                                                         RESULT 1
                                                                                                                                                                                                                  AAW3236
  Ada 22137 Mycobacte
Aag 1110 Mycobacte
Aag 14830 Mycobacte
Aae 29703 Mycobacte
Aae 29703 Mycobacte
Aae 1756 Mycobacte
Aae 1757 Mycobacte
Ada 26372 Mycobacte
Ada 26354 Mycobacte
Ada 26370 Mycobacte
                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacte
Mycobacte
M. tuberc
                                                                                                                                                                                                                                                                                                                                                                                                                                  M. tuberc
M. tuberc
M. tuberc
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aae29701 Mycobacte
Aae17565 Mycobacte
Aay05000 Mycobacte
                                                                   (without alignments)
2747.774 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                    1802
1 MSNSRRRSLRWSWLLSVLAA.....QTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                          Aaw81670 M.
                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                          June 30, 2004, 16:39:00 ; Search time 36.5039 Seconds
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Aay39109 N
Aau01890 N
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                  1586107 segs, 282547505 residues
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                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         protein search, using sw model
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AAE17565
AAY05000
AAO22137
AAG81110
AAY04830
AAE29702
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AAE17567
ADA26372
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ADA26356
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AAW38972
AAY39109
AAU01890
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AAW32435
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s: *
geneseqp2000s: *
geneseqp2001s: *
geneseqp2002s: *
geneseqp2003ss: *
geneseqp2003bs: *
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length: 2000000000
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Match 1
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Example 3; Page 114-116; 168pp; English
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                                                                                                                                          PQVVNINIYKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
                                                                                                                                                                                                                            QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMYTAASDNFQLSQGGQGFA 240
                                                                                                                                                                                                                                               IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
                                                                                                                                                                                                                                                           9
                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis.
                                                                                                                                                                                  121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
                                                                                                    1 MSNSRRRSIRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
especially monoclonal antibodies or equivalent polyclonal antibodies, also used for diagnosis
                                                                                                                                                                                                         QASDSLIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGFA
                                                                    Gaps
                                                                                                                                                                                                                                                                                     GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                               GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis; non specific adjuvant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houghton R;
                                                 Length
                                                                   Indels
                                               Score 1802; DB 2;
Pred. No. 7.2e-126;
                                                                    .
0
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                                       100.0%; Scc.
100.0%; Pred. No. ..
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis antigen TbRa35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC,
DR;
                                                                                                                                                                                                                                                                                                                                                         protein; 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00533634.
96US-00620874.
96US-00659683.
96US-00680574.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; immunogen; vaccine;
skin testing; M.tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                         Best Local Similarity 100.
Matches 355; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YA,
I, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-192903/17.
N-PSDB; AAT91477.
                                                                                                                                                                                                                                                                                                                                                        standard;
                             Sequence 355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
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Vedvick TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1997
                                                                                                                                              61
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                                                 Query Match
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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tubarculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TDRa35. The immunogenic protein, and fusion proteins containing one or more of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
                                                                                                                                                                                                                                                                                                                                                                        PQVVVINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                             YDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
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                                                                                                                                                                                                                          Length 355;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tuberculosis; infection; diagnosis; antigen; TbRa35.
                                                                                                                                                                                                                      Query Match 100.0%; Score 1802; DB 2; Best Local Similarity 100.0%; Pred. No. 7.2e-126; Matches 355; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis antigen TbRa35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis; strain H37Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dillon DC, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW64307 standard; protein; 355
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97US-00818111.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
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                                                                                                                                                                                     Sequence 355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-OCT-1997;
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13-MAR-1997;
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                                                                                                                                                 prevention)
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09-NOV-1998
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This polypeptide comprises Mycobacterium tuberculosis soluble antigen TDRa35. It is encoded by a DNA sequence (see AA444355) isolated from a M. tuberculosis strain H37Ra expression library with rabbit anti-sera raised against M. tuberculosis supernatar. No significant homology was found between TDRa35 and Genebank database sequences. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAM64291-W64379) compositions and methods for diagnosing tuberculosis. It provides soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using the above colypeptides, antibodies or oligonacleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QASDSLIGAEETINGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGFA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YDRIQDVAVLQIRGAGGLPSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGQIV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1802; DB 2;
100.0%; Pred. No. 7.2e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. tuberculosis immunogenic polypeptide TbRa35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                      Example 3; Page 115-116; 250pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 355; Conserv
N-PSDB; AAV44355
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 355 AA;
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Indels

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Length 355;

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YDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV 180
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                                                                                                                                                                                     Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
                                                                                                                                                                                                                                                                     This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method inducing protective immunity against tuberculosis (TB). This sequence be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSNSRRRSLRWSWILLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                        Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. tuberculosis recombinant antigen protein TbRa35.
                                                                                                                                                                                                                                                                                                                                                                                                  Score 1802; DB 2;
Pred. No. 7.2e-126;
                                                                                                          Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 7.2
Matches 355; Conservative 0; Mismatches
                                                                                                                                                                                                                                                Example 3; Page 110-111; 230pp; English
                                                                                                          Skeiky YAW, Dillon DC, C.
, Twardzik DR, Lodes MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; protein; 355
                                       96US-00730510.
97US-00818112.
             97WO-US018293
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                                                                                                                                                                                                                                                                                                                                                of tuberculosis
                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                   WPI; 1998-261042/23.
N-PSDB; AAV64463.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-1999
              07-OCT-1997;
                                         11-OCT-1996;
13-MAR-1997;
                                                                                                           Reed SG, Sk
Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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99WO-US003268

tuberculosis.

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Mycobacterium
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                                                                                                                                                                                                                                                                             This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSNSRRRSIEWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDBSAWVAQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                             Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Ho
Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1802; DB 2;
100.0%; Pred. No. 7.2e-126;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                      Example 3; Page 151-153; 323pp; English.
                                                    99WO-US003265
                                                                            98US-00024753
98US-00072596
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 355; Conservative
                                                                                                                                                                                     WPI; 1999-527416/44.
N-PSDB; AAZ19053.
                                                                                                                    (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 355 AA;
WO9942118-A2
                                                   17-FEB-1999;
                                                                            18-FEB-1998;
05-MAY-1998;
                         26-AUG-1999
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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M tuberculosis Ag's. M tuberculosis Ag's. My take encoding them, derived fusion proteins and other by decinings to generate a protective or therapeutical compositions or tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AZ1949 to AAZ19460 and AAX39083 to AAY39225 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
                                                                                                                                                                                                                                                                                                                                             New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQVVNINTKLGYMAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGOTYGVDVVG
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0
                                                                                                                                                       Campos-Neto A, Houghton R; I, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1802; DB 2;
100.0%; Pred. No. 7.2e-126;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 108-109; 299pp; English
                                                                                                                                                       lon DC, Ca
Lodes MJ,
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                                                                                                                                                    Dillon
                             98US-00072967
98US-00025197
                                                                                                                                                                               Jedvick TS, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 355; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention
                                                                                                                                                       Skeiky YAW
                                                                                                                                                                                                                                             WPI; 1999-527409/44.
N-PSDB; AAZ19265.
                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 355 AA;
                                 05-MAY-1998;
                                                                                                                                                       Reed SG,
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Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.

M. tuberculosis antigen TbRa35 amino acid sequence.

(first entry)

AAY39109 standard; protein; 355

AAY39109

Vaccine; immunity; diagnostic agent; gene therapy; MTB32A antigen;

Mycobacterium tuberculosis,

WO200272792-A2

Mycobacterium tuberculosis MTB32A antigenic protein.

(first entry)

27-JAN-2003 ÀAE29701;

AAE29701 standard; protein; 355 AA

AAE29701

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Dillon DC, Lodes ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens.
                                                                                                  TbRa35; Mtb32A; antigen; vaccine; tuberculosis; AIDS; acquired immunodeficiency disease.
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                                                  M. tuberculosis antigen TbRa35 (Mtb32A)
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99US-0158425P,
                                                                                                                                                                                 Mycobacterium tuberculosis.
(first entry)
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  29-AUG-2001
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The sequence represents Mycobacterium tuberculosis TDRa35 (also known as Mtb32A), an M. tuberculosis antigen. Compositions comprising at least 2 feterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease, AIDS

New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.

Guderian J;

Skeiky Y, Brannon M, WPI; 2002-759844/82.

N-PSDB; AAD47076.

(CORI-) CORIXA CORP.

13-MAR-2002; 2002WO-US008223. 13-MAR-2001; 2001US-0275837P Disclosure; Page 78-79; 155pp; English.

Sequence 355 AA;

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100.0%; Score 1802; DB 4; Length 355; 100.0%; Pred. No. 7.2e-126; ive 0; Mismatches 0; Indels 0
                                    Matches 355; Conservative
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RESULT 8

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polymerication sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, MIS, and 6H polymucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are wiseful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis WTB32A antigenic protien. WTB32A is also referred to as
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Matches 355; Conservative
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us-09-597-796c-4.rag

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Weobacterium species antigens, uncleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with the serological sensitivity of sera from individuals infected with the serological sensitivity of sera from individuals infected with treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune nesponse in a mammal, e.g., human, prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral mycobacterium, in vitro and in vivo assays for detecting humoral infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a immunogens to generate or elicit a protective immune response in a naminal. Sequences of the invention are useful as in vivo diagnostic agents for for intradermal skin test. The present sequence is Mycobacterium species manal manal skin test. The present sequence is Mycobacterium species
 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
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                   355
                                                                                               Fusion protein; antigen; serological sensitivity; immune response;
tuberculosis; infection; vaccine; MTB32A; Ra32FL protein.
                                                                         GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA
                                                                                                                                                                                                                                                                                                                      Mycobacterium species MTB32A (Ra35FL) protein.
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                                                                                                                                                                                                      AAE17565 standard; protein; 355 AA
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01-FEB-2001; 2001US-0265737P.
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N-PSDB; AAD28335.
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                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium sp.
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99.4%; Score 1792; DB 2; Length 355;

Query Match

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Gaps

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Length 355; Indels

Query Match
100.0%; Score 1802; DB 5;
Best Local Similarity 100.0%; Pred. No. 7.2e-126;
Matches 355; Conservative 0; Mismatches 0;

MTB32A (Ra32FL) protein

Sequence 355 AA;

ö Gaps ; 99.4%; Pred. No. 4e-125; iive 0; Mismatches 2; Indels 353; Conservative Best Local Similarity Matches 353; Conserv

240 300 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120 POVVNINITIGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV 180 121 YDRTÓDVAVLÓLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGOGGTPRAVPGRVVALGOTV 180 181 QASDSLTGAEFILNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGGFA 240 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300 MSNSRRRSIRWSWILSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA 60 1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVG 60 QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGGFA IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355 61 121 241 61 181 301 8 염 ਨੇ 유 8 셤 à ద à

RESULT 11

AA022137 standard; protein; 355

AA022137;

03-OCT-2002 (first entry)

Mycobacterium tuberculosis MTB32A protein.

vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; immunogen; cytokine.

Mycobacterium tuberculosis.

WO200125401-A2.

12-APR-2001

06-OCT-2000; 2000WO-US027652

99US-0158585P 07-0CT-1999;

(CORI-) CORIXA CORP.

Skeiky Y, Guderian J;

WPI; 2001-266299/27. N-PSDB; AAL40768 Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Disclosure; Fig 1; 39pp; English

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polymuclectide sequence of Ral2, a 14 kDa C-terminal fragment of serine protease antigen MTB32A of Mycobacterium tuberculosis, and a heterologous polymuclectide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum

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antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This sequence represents the Mycobacterium tuberculosis MTB32A protein
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 99.4
les 353; Conservative
                                                                                                                                                                                                                                                                                          Sequence 355 AA;
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RESULT 12 AAG811

AAG81110 standard; protein; 355 AA

AAG81110;

(first entry) 04-SEP-2001

Mycobacterium tuberculosis potential drug target protein SEQ ID 161.

Drug target; growth; organism viability; characterisation.

Mycobacterium tuberculosis.

WO200135317-A1

17-MAY-2001

13-NOV-2000; 2000WO-US031152.

12-NOV-1999; 99US-0165086P. 12-NOV-1999; 99US-0165124P. 01-FEB-2000; 2000US-0179531P.

(REGC) UNIV CALIFORNIA.

Marcotte EM; Rotstein SH, Eisenberg D,

WPI; 2001-329193/34. N-PSDB; AAH51961.

Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship

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Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated
                                                                                                                                                                                                                                                                            Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine; immunity; diagnostic agent; gene therapy; Ra35 antigen.
                                                      Guigueno A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis mature Ra35 antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1792; DB 2;
Pred. No. 4.3e-125;
                                                    Pelicic V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                 Mycobacterial DNA vectors containing
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                                                  Lim E,
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                                                                                                                                                                                                                                        Claim 32; Fig 50F; 309pp; French.
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                                                                    Goguet De La Salmoniere
                                                  Portnoie D,
            (INSP ) INST PASTEUR
                                                                                                        WPI; 1999-181045/15.
                                                                                                                                                                                                     protein expression.
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                                                                                                                           N-PSDB; AAX34252.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 379 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polypucleotide sequences AdHS1947 - AAHS2092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PQVVNINTKLGYNNAVGAGTGIVIDENGVVLTNNHVIAGATDINAFSVGSGGTYGVDVVG 120
between nucleotide or polypeptide sequences, and comparing the sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection.
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                                                                                                                                                                                                                                                                                                                                                                                         Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                     Score 1792; DB 4;
Pred. No. 4e-125;
); Mismatches 2
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                                    Disclosure, Page 157; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY04830 standard; protein; 379
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                                                                                                                                                                                                                                                                                                                                                                                     99.4%;
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97FR-00011325.
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Matches 353; Conservative
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11-SEP-1997;
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Length 379; Indels 60 84 120 144 180 240

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                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGABETLNGLIQFDAAIQPGDSGGPV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 VVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETINGLIQFDAAIQPGDSGGPV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 79-80; 155pp; English.
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                                                                                                                                                                                                            Guderian J;
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                                                                  13-MAR-2002; 2002WO-US008223
                                                                                                             13-MAR-2001; 2001US-0275837P.
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                                                                                                                                                                                                            Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                       WPI; 2002-759844/82.
N-PSDB; AAD47077.
                                                                                                                                                                (CORI-) CORIXA CORP.
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                      19-SEP-2002
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, consention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the attibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human continual sequences of the invention are also used as vaccines. MTB32A fusion proteins skin test. The present sequence is Mycobacterium species mTB32A (MTB32A) (MTB32A) mature protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
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                                                                                                                                                                                                                                                                                   /note= "Ra35 C-terminal peptide, Ra12"
                                                                                                                                                                          /note= "Ra35 N-terminal peptide"
                                                                                                                                                                                                               /note= "Encoded by GAG"
                                                                                                                                                                                                                                                'note= "Encoded by
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01-FEB-2001; 2001US-0265737P.
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les 321, Conservative
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Sal L

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Fusion protein, antigen, serological sensitivity, immune response; tuberculosis, infection, vaccine, MTB32A, Ra32FL protein.

Location/Qualifiers

Mycobacterium sp.

Mycobacterium sp. MTB32A (Ra35FL) mature protein.

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Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-151;
Matches 355; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: sin

; TOPOLOGY: linear

US-08-818-112-79
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1 MSNSRRRELRWSWLLSVLAA.....QTKSGGTRTGNVTLAEGPPA 355
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-818-111-80
US-09-075-596-80
US-09-072-596-79
US-09-287-499-2
US-09-287-499-2
US-09-287-849-2
US-09-287-849-2
US-09-88-818-111-67
US-09-056-556-66
US-08-918-111-67
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US-09-68-118-815
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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Maximum DB
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Bkeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Unions Net, Manch C.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Trandzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: G300 Columbia Center, 701 Fifth Avenue
                        Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-AAR-1997
CLASSIFICATION: 424
ATYONENY/AGENT INPORMATION:
NAME: MAK: DAVIG J: 1392
RESTRENCE/DOCKET NUMBER: 31,392
RESTRENCE/DOCKET NUMBER: 31,392
RESTRENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION OF 79:
SEQUENCE CRARACTERISTICS:
INPORMATION FOR SEQ ID NO: 79:
SEQUENCE CRARACTERISTICS:
LENGTH: 355 anino acids
                        US-09-636-215-852
US-09-681-166A-852
US-09-691-12C-349
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US-09-598-419-349
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US-08-318-112-79
Sequence 79, Application US/08818112
Patent No. 6290969
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CITY: Seattle
STATE: Washington
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                                                            1 MSNSRRRSLRWSWILLSVLAAVGLGLATAPAQAAPPALSODRFADFPALPLDPSAMVAOVA
                                                                                                                   61 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG
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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1802; DB 4; Best Local Similarity 100.0%; Pred. No. 2.1e-151; Matches 355; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David,
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFRAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-056-556-79

Sequence 79, Application US/09056556

Patent No. 6350456

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION:
COMPOUNDS AND M.
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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US-09-056-556-79
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                                                                                   PQVVNINTKLGYNNAVGAGTGIVIDPNGVVJTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
                                                                                                            61 PQVVNINTKLGYNNAVGAGTGIVIDFNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
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MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA 60
                           121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
                                                                                                                                                                                                                                                                                                                                                                                 241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
                                                                                                                                                                        YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Breiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Uedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: GAIO Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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100.0%; Score 1802; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.1e-151;
Matches 355; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 355 amino acids
amino acid
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MEDIUM TYPE: Floppy
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Washington
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US-08-818-111-80
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STATE: Wa
COUNTRY:
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US-08-818-111-80
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                                                                                                                                               121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV 180
                                                                                                                                                                            121 YDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGQTV 180
                                                                                                                                                                                                                                               181 QASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGNNTAASDNFQLSQGGQGFA 240
                                                                                                                                                                                                                                                                                                                                                                                            241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
                                                                                                                                                                                                                                                                                                                                               241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campes-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardix, Thomas S.
APPLICANT: Twardix, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONDITY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLLASSIPICATION:
NAME: Maki, David J.
REGISTRATION:
REFERENCE/POCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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6300 Columbia Center, 701 Fifth Avenue
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Patent No. 6458366
GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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STATE: Washingt
COUNTRY: USA
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CITY: Se
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61 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
                                                                                                                                       61 PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
                                                                                                                                                                                                                     121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV 180
                                                                                                                                                                                                                                                   181 QASDSLIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA 240
                                                                                                                                                                                                                                                                                                                                                                                 181 QASDSLIGAEBTINGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGFA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
1 MSNSRRRSIRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDFDSAMVAQVA 60
                                 1 MSNSRRRSLRWSWILLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDDPSAWVAQVA 60
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Wardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: APPLICANT: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
SOFTWARE:
SOFTWARE:
PARENTIN Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFTCATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 79, Application US/09072967 Patent No. 6592877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (206) 622-4900
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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amino acid
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TOPOLOGY: lin
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GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGV 147
                                                                                                                                                                          SGGPVVNGLGQVVGMNTAAS 596
                                                                                                                                                 208 SGGPVVNGLGQVVGMNTAAS 227
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                                                                                                                                                                                                                                                                     Sequence 2, Application US/09223040 Patent No. 6544522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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SEQ ID NO 2
LENGTH: 729
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fuelon Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: And Their Uses
FILE REFERENCE: 014058-00902003
FURRENT APPLICATION NUMBER: US 08/9112
PRIOR APPLICATION NUMBER: US 08/9112
PRIOR APPLICATION NUMBER: US 08/92,578
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 26
                                                                                                                                           PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
                                                                                                                                                                    61 PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
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                                                                                            1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
                                                                                                                                                                                                                                                                                    181 QASDSLITGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMWTAASDNFQLSQGGGFA
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                                       Gaps
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                                   0;
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; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
US-09-287-849-26
     Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 983; DB 4; Length 596;
Pred. No. 1.1e-78;
0; Mismatches 5; Indels
                                     Indels
Query Match 100.0%; Score 1802; DB 4; Best Local Similarity 100.0%; Pred. No. 2.1e-151; Matches 355; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/09287849 Patent No. 6627198
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Best Local Similarity 97.5%;
Matches 195; Conservative C
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GENERAL INFORMATION:

APPLICANT: Skeiky; Yasir
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa, Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 01408-009010US
CURRENT APPLICATION NUMBER: US/09/223,040
CURRENT FILING DAFE: 1998-12-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-287-849-2

Sequence 2, Application US/09287849

Sequence 2, Application US/09287849

Sequence 2, Application US/09287849

Sequence 2, Application:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Asir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Coriso Corporation

TITLE OF INVENTION: Rusion Proclems of Mycobacterium tuberculosis Antigens

TITLE OF INVENTION: and Their Uses

FILE REFERENCE: 014058-009020US
                                                                                                     517 AVGEPVVAMGNSGGGGGTPRAVPGRVVALGGTVQASDSLTGAEETLNGLIQFDAAIQPGD 576
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                                                              AVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 APAQAAPPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-223-040-2
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David V.
REGISTRATION NUMBER: 31,392
REFERENCE/LOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-818-111-67
; Sequence 67, Application US/08818111
; Patent No. 6338852
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INFORMATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 TGNVTLAEGPPA 355
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                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-818-112-66
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.6%; Score 983; DB 4; Length 729; Best Local Similarity 97.5%; Pred. No. 1.5e-78; Matches 195; Conservative 0; Mismatches 5; Indels
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
  CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR PELING DATE: 1999-04-07
PRIOR PILING DATE: 1997-03-13
PRIOR PLING DATE: 1997-10-01
PRIOR PLING DATE: 1997-10-01
PRIOR PILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN Ver. 2.1
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ORGANISM: Artificial Sequence
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TUBERCULOSIS 9 224 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGAR 1 TAASDNFQLSQGGQFAIPIGQAMAIAGQIRSGGGSPTVHIGFTAFLGLGVVDNNGNGAR APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Shollon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Howork, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue Query Match 37.5%; Score 676; DB 3; Length 132; Best Local Similarity 100.0%; Pred. No. 2e-52; Matches 132; Conservative 0; Mismatches 0; Indels STREET: Below COLUMBIA CHILCE, FILL STREET: BELOWING COUNTRY: USA 212: 99104-7092
ZIP: 99104-7092
ZIP: 99104-7092
COMPUTER READABLE FORM: MEDIUM TYPE: FLORMY disk COMPUTER: IBM PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/818,111
FILING DATE: 13-MAR-1997
CLLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION: NAME: Maki, David J. REGISTRATION: WAS MEDISTRATION: 424
ATTORNEY/AGENT NUMBER: 210121.417C6
TELECHOMORICATION INFORMATION: TELECHOMORICATION INFORMATION INFORMATION INFORMATION: TELECHOMORICATION INFORMATION
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61 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTR 120
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Vedvick, Thomas ...
Vedvick, Thomas ...
Twardzik, Daniel R...
Lodes, Michael J...
Hendrickson, Ronald C...
Hendrickson, Ronald C...
**Tentrickson, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PSTETM: PC compatible
OPERATING SYSTEM: PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
TITING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/09072596
Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 21 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS:
                                                                                        344 TGNVTLAEGPPA 355
                                                                                                                                                                   121 TGNVTLAEGPPA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 TGNVTLAEGPPA 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lodes, Mich
APPLICANT: Hendricksor
TITLE OF INVENTION: CC
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: Sir
TOPOLOGY: linear
US-09-072-596-67
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STATE: Washing
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STREET: 63
                                                                                                                                                                                                                                                                                                                                           US-09-072-596-67
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US-09-072-967-66
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                                                                                                                                                                                                                                                                                              Gaps
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                      Query Match 37.5%; Score 676; DB 4; Length 132;
Best Local Similarity 100.0%; Pred. No. 2e-52;
Matches 132; Conservative 0; Mismatches 0; Indels
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ZUE: 98104-7022

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 21,312.457
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
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Matches 132; Conservative
                              STRANDEDNESS: single;
TOPOLOGY: linear
US-08-818-111-67
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ADDRESSEE: SEED and I
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amino acid
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US-09-056-556-66
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61 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTR 120
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APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Reter. Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: CONFOSTIONS OF PROSTATE CANCER

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE

CURRENT APPLICATION NUMBER: US/09/636,215

CURRENT FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 852

SOFTWARE: FastSEQ for Windows V-

SEQ ID NO 819

LENGTH: 132

TYPE: PPT
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Sequence 848, Application US/09636215
Patent No. 6620922
GENERAL INCRMANTION:
GENERAL INCRMANTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-636-215-819
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                       APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
ITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.5%; Score 676; DB 4; Length 132; Best Local Similarity 100.0%; Pred. No. 2e-52; Matches 132; Conservative ,0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: 8330 COLUMNIA CENCET, 701 FILLI AVENUE
STATE: Washington
COUNTRY: USA
ZUP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYRE: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKE: MAKE: David J.
REGISTRATION NUMBER: 210121.411C9
TELEFRATION NUMBER: 21031.411C9
TELEFRATION OF SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                   ; Sequence 66, Application US/09072967; Patent No. 6592877; GENERAL INFORMATION: APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 TGNVTLAEGPPA 355
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: LONGOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.42717C17
FILE CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT APPLICATION NUMBER: US/09/636,215
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 848 LENGTH: 132

US-09-636-215-819

RESULT 14

; TYPE: PRT ; ORGANISM: Homo sapiens US-09-636-215-848

0; Gaps Query Match 37.5%; Score 676; DB 4; Length 132; Best Local Similarity 100.0%; Pred. No. 2e-52; Matches 132; Conservative 0; Mismatches 0; Indels

224 TAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGFPAFLGLGVVDNNGNGAR 283

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284 VQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVLSVNWQTXSGGTR 343

344 TGNVTLAEGPPA 355 ||||||||||||| 121 TGNVTLAEGPPA 132

Search completed: June 30, 2004, 16:55:18 Job time: 11.7991 secs

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June 30, 2004, 16:52:58; Search time 27.6821 Seconds (without alignments) 3625.462 Million cell updates/sec
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1 MSNSRRRSLRWSWLLSVLAA......QTKSGGTRTGNVTLAEGPPA 355
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 79, Appl Sequence 79, Appl Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 20, Appli Sequence 20, Appli Sequence 2, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli	
ΩΙ	US-09-886-349A-2 US-10-193-002-80 US-10-084-843-79 US-10-088-732A-2 US-09-712-363-161 US-09-712-363-161 US-09-886-349A-4 US-10-369-983-19 US-10-098-732A-6 US-10-098-732A-6 US-10-098-732A-6 US-10-369-983-2 US-10-369-983-2 US-10-369-983-4 US-10-369-983-16 US-10-369-983-16	
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828 1022 1952 1955	66666666666666666666666666666666666666	0 0 0 0 0 4 4 4 8 R	132 132 132 132 132 132 132 132 132 132
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                                                                                              61 PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
                                                                                                                                         61 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
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    MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDFSAMVAQVA
                                            1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION NUMBER: US/09/072,967
APPLICATION NUMBER: US/09/072,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Neto, Antonio
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,392
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STATE: Washington
COUNTRY: USA
CLIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
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TELEFAX: (206) 682-6031
N FOR SEQ ID NO: 79:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 79, Application US/10084843 Publication No. US20030143243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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                                       121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV
                                                                                       QASDSLIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFA
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100.0%; Score 1802; DB 14; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 355; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Netc, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10--7ul-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-193-002-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 80, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 355 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 350
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STATE: Washington
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US-10-193-002-80
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181 QASDSLFGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGGF 240
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                                                                                                                                                                                                                                                           1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPLPLPLDFSAMVAQVA 60
                                                                                                                                                                                                                                                                                          1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA 60
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Publication No. US20030175294A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Golfrey
APPLICANTON NUMBER: US 40/10/098,732A
CURRENT APPLICATION NUMBER: US 60/275,837
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR APPLICANTON NUMBER: US 60/275,837
SEQ ID NO: SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 355
                                                                                                                                                                                                0; Indels 0; Gaps
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                                                                                                                                     Query Match 100.0%; Score 1802; DB 14; Length 355; Best Local Similarity 100.0%; Pred. No. 1.6e-134; Matches 355; Conservative 0; Mismatches 0; Indels 0;
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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-084-843-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mycobacterium tuberculosis
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US-10-098-732A-2
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US-10-098-732A-2
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 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300

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Sequence 161, Application US/09712363 Sequence 161, Application US/09712363 Sequence 161, Application US/09712363 Sequence 161, Application US/09712363 SERVENCE 1020001648901 APPLICANT: Resteria, Sergio H. APPLICANT: Marcotte, Edward M. TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND TITLE OF INVENTION: DETERMINING THE FUNCTIONS OF PROTEINS SY COMPARATIVE ANALYSIS FILE REPERMORE: 07419-03200.11-13 CURRENT FILING DATE: 2000-11-13 ENGINE PELICATION NUMBER: 06/179,531 PRIOR FILING DATE: 2000-01-2 PRIOR FILING DATE: 2000-01-2 PRIOR FILING DATE: 2000-02-01 PRIOR FILING DATE: 2009-03-04 PRIOR PELICATION NUMBER: 06/113,409 PRIOR PELICATION NUMBER: 06/113,409 PRIOR PELICATION NUMBER: 06/113,093 PRIOR PELICATION NUMBER: 06/113,093 PRIOR PELICATION NUMBER: 06/165,124 PRIOR PELICATIO	61 PQVVNINTRIGGGRANDAVGAGTGIVIDENGVVLINNHVIAGATDINAFSVGSGGITGVDVVG 121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGGTV 121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGQTV	181 QASDSLIGABETLNGLIQFDAAIQPGDSGGFVVNGLGQVVGMYTAASDNFQLSQGGGFA
SULT 5 -09-712-163- Sequence 161 BREEFEL INPO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF IN TITLE TITLE OF IN TITLE T		_

1 MSNSRRRSLRWSWILSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAWVAQVA 60

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121 YDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV 180

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248 GVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVIS 307
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                                                                                           Fusion Protein Constructs Comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 APPALSODRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 APPALSQDRFADFPALFLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 NNHVIAGAIDINAFSVGSGQTYGVDVVGYDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 NNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEP
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Publication No. US20030235593A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Gree, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING. DATE: 2002-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:Ra35 mature
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                             APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
TITLE OF INVENTION: Heterologous Fusion Prote
TITLE OF INVENTION: Heterologous Fusion Prote
FILE REFERENCE: 014058-0120100S
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT APPLICATION NUMBER: US 60/275,837
PRIOR PILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 4
SEQ ID NO 4
LENGTH: 330
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.4
Matches 321; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 330
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                                                     IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST
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                                                                                                                                                                                      GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/0986349A
; Publication No. US20040086523A1
; REMEAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Skeiky, Yasir
; APPLICANT: Reed, Steven
; APPLICANT: Aderson, Mark
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
; TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
; TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
; CURRENT APPLICATION NUMBER: US 09/597,796
; PRIOR APPLICATION NUMBER: US 69/597,796
; PRIOR FILING DATE: 2000-06-20
; PRIOR FILING DATE: 2001-06-20
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH 2300
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; OTHER INFORMATION: MTB32A (Ra35 mature)
US-09-886-349A-4
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RESULT 11
US-10-369-983-20
Sequence 20, Application US/10369983
Publication No. US20030235593A1
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; Sequence 6, Application US/09886349A
; Publication No. US20040086523A1
; GENERAL INFORMATION:
    APPLICANT: Skeiky, Yasir
    APPLICANT: Reed, Steven
; APPLICANT: Reed, Steven
; APPLICANT: Reed, Steven
; APPLICANT: Corixa Corporation
    ITILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; TITLE REFERENCE: 014058-009070US
; CURRENT APPLICATION NUMBER: US/09/886,349A
; CURRENT FILING DATE: 2001-06-20
; RICR APPLICATION NUMBER: US 09/597,796
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 50
; SOGTWARE: PatentIn Ver: 2.1
; SOGTWARE: PatentIn Ver: 2.1
; LENGTH: 330
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                                               Query Match 90.7%; Score 1634; DB 15; Length 330; Best Local Similarity 99.4%; Pred. No. 2.9e-121; Matches 321; Conservative 0; Mismatches 2; Indels 0;
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US-09-886-349A-6
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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderlaid, deffrey
APPLICANT: Guderlaid, deffrey
TILE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TILE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TILE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TILE OF INVENTION: Heterologous Fusion
FILE REPRENCE: 014058-01201008
CURRENT FILING DATE: 2001-03-03
FRIOR APPLICATION NUMBER: US 60/275,837
FRIOR APPLICATION NUMBER: US 60/275,837
FRIOR FILING DATE: 2001-03-13
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 6
LENGTH: 330
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                                                                        188 VNGLGQVVGMNTAASDNFQLSQCGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTFLGL
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213 VNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL
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JEDNICALINFORMATION:

JAPPLICANT: SKEINY, Yasir

APPLICANT: Guderian, Jeff

APPLICANT: Reed, Steven

JITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

CURRENT FILING DATE: 2003-02-18

MUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 723

TWODE: DON 1
          APPLICANT: Skelky, Yasir
APPLICANT: Skelky, Yasir
APPLICANT: Gudeklan, Jeff
APPLICANT: Gudeklan, Jeff
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US 10/10/369,983
CURRENT FILING DATE: 2002-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
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ORGANISM: Artificial Sequence
GENERAL INFORMATION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10369983
PUDIcation No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Corixa Corporation
APPLICANT: Responsion
FILLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERBNCE: 014058-09081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT APPLICATION NUMBER: US 60/357,351
FRICK APPLICATION NUMBER: US 60/357,351
FRICK APPLICATION DATE: 2002-02-18
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                                                                                                                                      Length 723;
, OTHER INFORMATION: Description of Artificial Sequence:mutated , OTHER INFORMATION: MTB32-MTB39F fusion protein (MTB32MutSA) US-10-369-983-2
                                                                                                                                                                                                   Indels
                                                                                                                               Query Match 90.5%; Score 1631; DB 15;
Best Local Similarity 99.1%; Pred. No. 1.3e-120;
Matches 320; Conservative 1; Mismatches 2;
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188 VNGLGGVVGMTAASDNFQLSQGGGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 247
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                                                    213 VNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGL 272
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128 VVAMGNSGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPV 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: fusion protein OTHER INFORMATION: MTB103F (MTB72F-85b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Greven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
CURRENT APPLICATION WUMBER: 2003-02-18
FRICA APPLICATION NUMBER: US 60/357,351
PRIOR PELING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 55.5%; Score 999.5; DB 15; Length 1016; Local Similarity 84.1%; Pred. No. 2e-70; es 207; Conservative 6; Mismatches 18; Indels 15;
                                                                                                                                                                                                                                                                     333 VNWOTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                      308 VTWOTKSGGTRTGNVTLAEGPPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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US-10-369-983-16
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US-10-369-983-18
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LENGTH: 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       590 GVVLTINNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGV 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 AFLGLGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPI--NSATAMADALNGH 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 SGGPVVNGLGQVVGNNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 APAQAAPPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPN 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 AVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence:fusion protein; OTHER INFORMATION: MTB114F (MTB72F-mTCC#2)
US-10-369-983-16
              APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
TITLE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR PILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 HPGDVISVNW-------QTKSGGTRTGNVTLAEGPPA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :: | | :: | | 804 -----VGWLAATAALAKETATQARAAAEAFGTAFAMTVPPS 839
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
55.0%; Score 992; DB 15;
Best Local Similarity 63.8%; Pred. No. 9.2e-70;
Matches 219; Conservative 17; Mismatches 59;
                                                                                                                                                                                                                                        LENGTH: 1154
TYPE: PRT
ORGANISM: Artificial Sequence
APPLICANT: Reed, Steven
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                                                                                                                                                                                                                                                                                                              FEATURE:
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Search completed: June 30, 2004, 17:14:43 Job time : 28.6821 secs

Sequence 16, Application US/10369983; Publication No. US20030235593A1; GENERAL INFORMATION: APPLICANT: Skeiky, Yasir; APPLICANT: Guderian, Jeff

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OM protein - protein search, using sw model

June 30, 2004, 16:43:31; Search time 9.27806 Seconds (without alignments) 3680.509 Million cell updates/sec Run on:

US-09-597-796C-4 1802 1 MSNSRRRSLRWSWLLSVLAA.....QTKSGGTRTGNVTLAEGPPA 355 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SUMMAKLES	
Result No.	Score	Query Match	Length	DB	Д	Description
		1 6	35	5	F70983	probable serine pr
Ŋ	1306	ď	36	7	S47170	
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9	460	25.5	452	0	T45448	serine
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ω	7	。	40	7	AG2150	serine proteinase
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12	4	9.	45	0	AG0433	proteinase (EC 3.4
13	•	19.0	51	N	A82581	periplasmic protei
14	35.	8	42	Ŋ	AD1894	
15	3	18.4	41	N	AB2057	ď
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17	331	18.4	45	Ŋ	C91142	erine en
18	3	8	45	N	F85987	
19	٠	φ.	47	7	F83550	serine proteinase
20	329	18.3	39	N	B71284	Н.
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17.6									310 17.2			306 17.0			

ALIGNMENTS

RESULT 1 F70983 probable	1 e serine proteinase pepa - Mycobacterium tuberculosis (strain H37RV)
C;Specio C;Date: C:Boses	C.Species: Mycobacterium tuberculosis C.Jate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Dec-2002 C.Accesion: P70083
R;Cole, S.T.; ; Connor, R.;	
Kajandream, Nature 393,	kajandream, m.A.; kogers, J.; kurter, S.; beeger, N.; skerton, S.; squares, S. Nature 393, 537-544, 1998
A; Autho: A; Title	A, Authors: Sqares, R.; Suiston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;itle: lociphering the biology of Mycobacterium tuberculosis from the complete genome &
A; kererence r A; Accession:	•
A;Statu: A;Molecu	A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A, Residi	A.Residues: 1-355 <col/> Kross-references: GB:256071; GB:AL123456; NID:g3242254; PIDN:CAB09453.1; PID:g2181967 A.Terneriamental source: strain H378v
C, Genetics:	
C; Superfamily	;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps
Query Best 1	tch 355; sal Similarity 99.4%; Pred. No. 7.5e-98;
Matches	3; Conservative 0; Mismato
Å.	1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFAALPLDPSAWVAQVA 60
qq	1 MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVG 60
ò	61 POVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
qq	61 PQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVG 120
λ̈	121 YDRTQDVAVLQLRGAGGLPSAALGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGQTV 180
ପ୍	121 YDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGQTV 180
δ	181 QASDSLTGAEETINGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGFA 240
qq	181 QASDSLTGAEETINGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGFA 240
à	241 IPIGQAMALAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
DÞ	241 IPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLGIST 300
ò	301 GDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLABGPPA 355
qa	301 GDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGPPA 355

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7; Gaps

57 28 117 117 237

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Cyaccesion: C70821
R;Cole, S.T.; Bercsch, R.; Parkill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Parkill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Anuthors. Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Reference number: Rollogy of Mycobacterium tuberculosis from the complete genome facesion: C70821
A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Reference number: DNA
A; Residues: preliminary: nucleic acid sequence not shown; translation not shown
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C,Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps
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                                                                                                                                                                                                                                                                                                                                                                                          118 VVGYDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                       GFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPAASLG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVLOLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable serine proteinase Rv0983 - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 ISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLARGPPA 355
                                                                                                            MSNSRRRSLRWSWLLSVLAAVGLGLATAPAQA----APPALSQDRFADFPALPLDPSAMVA
                                                                                                                                                      1 MSRQPHRSLWRSWLVSTLAALGLSLAVVPGSATPSGPSTLALDRFSNRPPLPLNPAAM--
                                                                                                                                                                                                                                                           58 QVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVD
                                                                                                                                                                                                                                                                                             QTVQASDSLTGAEETLNGLTQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 AVVRVQGVSGLTPISLGSSSDLRVGQPVLAIGSPLGLEGT - - VTTGIVSALNRPVSTTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 AAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSA---MVAQVAPQVVNINTKLGYNNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 LIGAEETLNGLIQFDAAIOPGDSGGPVVNGLGQVVGMVIA----ASDNFQLSQG--GQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 ISVGDIITSVDGVPISEATAMTNVLVPHHPGETVAVNYRSAGGGDLTANVTLAEGPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.0%; Score 468.5; DB 2; Length 464; 36.0%; Pred. No. 2.1e-20; tive 59; Mismatches 136; Indels 31
                                             Indels
1.7e-67;
ches 58;
           70.1%; Pred. No. 1.7e ive 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 VGAGTGIVIDPNGVVLTNNHVIAGAT---
           al Similarity 70.1%
251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 36.0
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178
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           Best Local
Matches 25
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RESULT 2
S47170
Sylvetical protein 34K - Mycobacterium paratuberculosis
C;Species: Mycobacterium paratuberculosis
C;Species: Mycobacterium paratuberculosis
C;Accession: 847170
S;Cybate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Dec-2002
C;Accession: 8.47170
S;Cybate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Dec-2002
S;Cybaterion: 8.47170
S;Cybaterion: Isolation and characterisation of a 34KDa protein of Mycobacterium paratumy
S;Reference number: 847170
S;Status: preliminary
S;Rolession: 847170
S;Status: DNA
S;Residues: 1-361 <CAM
S;Residues: 1-361 <CAM
S;Coss-references: BMBL:Z23092; NID:g505550; PIDN:CAA80638.1; PID:g505551
C;Superfamily: Escherichia coli trypsin-like proteinase degs; GLGF domain homology; tryp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3

A87242

probable secreted serine proteinase [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002

R;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002

R;Date: 20-Apr-2001

R;Davies, R.M.; Biglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Atille: Massive gene decay in the leprosy bacillus.

A;Afile: Massive gene decay in the leprosy bacillus.

A;Reference number: A86509; MUID:21128732; PMID:11234002

A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YAVDVVGYDRTQDIAVLQLRGAAGLPTATIGGEATVGEPIVALGNVGQGGTPNAVAGKV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 AAAGIAPGDVITGVDTVPINGATSWTEVLVPHHPGDTIAVHFRSVDGGERTANITLAEGP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-354 <STO>
A;Cross-references: GB:AL450380; NID:g13093863; PIDN:CAC32191.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML2659
C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 -GGGGFAIPIGRAMAVANQIRSGAGSNTVHIGPTAFLGLGVTDNNGNGARVQRVVNTGPA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 YGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 QGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSAPA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 ASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEGP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VALNQSVSATDTLTGAQENLGGLIQADAPIKPGDSGGPMVNSAGQVIGVDTAATDSYKMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSKSHHHRSVWWSWLVGVLTVVGLGLGLGSGVGLAPASAAPSGLALDRFADRPLAPIDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAASDNFQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSNS-RRRSLRWSWLLSVLAAVGLGL----ATAPAQAAPPALSQDRFADFPALPLDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 AMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AWYGQVGPQVVNIDTKFGYNNAVGAGTGIVIDPNGVVLTNMHVISGATEISAFDVGNGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.5%; Score 1306; DB 2; Length 361; 70.4%; Pred. No. 1.9e-69; Live 41; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 70.4
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA 355
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354

DB 2; Length 354;

70.6%; Score 1272.5;

Query Match

Db 355 AIPVDQAKRIADELISTGKASHASLGVQVTNDKDTLGAKIVEVVAGGAAANAGV 408 Qy 299 STGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAE 351	C,Genetics: A;Note: MLCB373.28 C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps C;Keywords: hydrolase; serine proteinase F;182,224,305/Active site: His, Asp, Ser #status predicted
RESULT 5 H86501 Figure 1	Query Match 25.5%; Score 460; DB 2; Length 452; Beet Local Similarity 36.4%; Pred. No. 6.38-20; Matches 130; Conservative 52; Mismatches 121; Indels 54; Gaps 12; Qy
;, GLGF domain ho 382;	33.9
130; Conservative 5: 22 GLGLATAPAQAAPPALSQDF	Db 393 NAAVPKGVVLTKVDDRLISSADALVAAVRSKAPCDKVŠLTYQDQSGSSR†VQVTLGK 449 RESULT 7
Qy 78 AGTGIVIDPNGVVLTNNHVIAGATDINAPSVGSGQTYGVDVVGYDR 123	S/4843 Syledys Proteinase hhoA (EC 3.4) - Synechocystis sp. (strain PCC 6803) N;Alternate names: protein s111679 C;Specises: Synechocystis sp. A:Variety: PCC 6803
	C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Dec-2002 C;Accession: S74643 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; R;Koumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
Oy 182 ASDSITGAEETINGLIOFDAAIOPEDSGEPVNGLGOVGWNTAASDNFQLSQG 235 1	DNA KeB. 3, 109-115, 1590 A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis A; Reference number: S74322; MUID:97061201; PMID:8905231 A; Accession: S74643 A; Status: nucleic acid sequence not shown; translation not shown
ovaldketpeda svnwotksegt :: : LTYODOSESS	A; Molecule type: DNA A; Residues: 1.394 KRAN> A; Residues: 1.394 KRAN> A; Residues: 1.394 KRAN> A; Cross-references: KRAN- A; Cross-references: Residues sequence was submitted to the EMBL Data Library, June 1996 C; Genetics: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C; Genetics: Aboba A; Gross-in Day C; Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps
RESULT 6 T45448 probable serine proteinase (EC 3.4.21) MLCB373.28 [similarity] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 31-Jan-2000 #text_change 09-Dec-2002	C;Keywords: nydrolase; protellase Query Match Best Local Similarity 31.6%; Pred: No. 2e-15; Matches 116; Conservative 50; Mismatches 117; Indels 84; Gaps 14;
C;Accession: T45448 R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1998 A;Reference number: Z22967	
A,Status: preliminary; translated from GB/EMBL/DDBJ A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA A,Residues: 1-452 < JAM> A,FResidues: 1-452 < JAM> A,FResidues: EffEL:AL035500; PIDN:CAB36690.1 A,FEXperimental source: cosmid L373	OY 58 QVAPQVVNINTK

RESULT 9 S77538 serine proteinase (EC 3.4.21) htrA - Synechocystis sp. (strain PCC 6803) N;Alternate names: protein slr1204 C;Species: Synechocystis sp. A;Variery: PCC 6803 C;Accession: S77538 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Ovmurra, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DN, Res. 3, 109-136, 1996 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis	A; Reference number: S74322; MUID:97061201; PMID:896 A; Accession: S77538 A; Status: nucleic acid sequence not shown; translat A; Molecule type: DNA A; Residues: 1-452 < KAN> A; Cross-references: EMBL:D90905; GB:AB001339; NID:9 A; Oross-references: EMBL:D90905; GB:AB001339; NID:9 A; Note: the nucleotide sequence was submitted to th C; Genetics: A; Gene: htrA C; Superfamily: Escherichia coli trypsin-like protei C; Keywords: hydrolase; serine proteinase Query Match Best Local Similarity 29.2%; Pred, No. 818-14	Matches 116; Conservative 65; Mismacches 129; Indels 87; Gaps Qy 16	LLSATGRRSADIGVPDKRVEFIGTDÄÄINPG LSQGQGGPAIPTGQANAIAGQIRSGGGSPTVHIGP LSGGGPAIPTNKAQEIAOQLIATGKVEHGIGFAIPTNKAQEIAOQLIATGKVEHGIGFALVUNSAPAASLGISTGDVITAVDG HIPVDKGVVNGWQWPNSPAAIKLEGFI-:- IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 10 H97199 htrA-like serine protease (with PDZ domain) [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium C;Species: Clostridium acetobutylicum C;Species: Clostridium C;Species: Clostr
	Oy 312 INSATAM 318 Db 350 ISDGARL 356 RESULT 8 AG2150 Serine proteinase [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AG3150 R;Kaneko, T:; Nakamura, Y:;Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Suginoto, M.; Takazawa, M.; Yanada, M.; Yasuda, M.; Tabata,	us Nitrogen-fixing Cyanobact 59840 ID:gl7l31851; GSPDB:GN00179 nase degs; GLGF domain homolc Length 407; 1; Indels 88; Gaps 15;	7 RSLRWSWILSVLAAVGLGLATAPAGAAPPALSQDRFADFPLD	189 PLGSSNNVQVGBWAIAVGNPLGFDNT

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S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erichia coli trypsin-like proteinase degS; GLGF domain homology; tryps
se; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL:D90905; GB:AB001339; NID:g1652360; PIDN:BAA17385:1; PID:g165246: ide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                             , 1990 nalysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GAGTGIVIDPNGVVLTNNHVIAGATDIN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQAFNDPFLQRFFGSQMPPMPNERVQRGTGSGFIVSNDGKIFTNAHVVDGADEVT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVPGRUVALGOTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ONFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVDNN---- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETGMNIPVDKGVVIMQVMPNSPAAIAKLEQGDVLQSLQGGPVENAEQVQSLVGKL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.7
                                                                                                   #sequence_revision 25-Apr-1997 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQV----APQVVNINTKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [EC 3.4.21.-) htrA - Synechocystis sp. (strain PCC 6803)
protein slr1204
ystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.7%; Score 355.5; DB 2; Length 452;
rity 29.2%; Pred. No. 8.1e-14;
nservative 65; Mismatches 129; Indels 87; Gaps
                                                                                                                                                                                                                                                                                                                                                 cid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                              S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISVNWQTKSGGTRTG---NVTLAEG----PP 354
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	19.0%; Score 343; DB 2; Length 457; 19.0%; Score 343; DB 2; Length 457; 19.0%; Pred. No. 4.4e-13; 19.1%; Pred. No. 4.4e-13;
A; Molecule type: DNA A; Residues: 1-433 skUR. A; Cross-references: GB.AE001437; PIDN.AAK80397.1; PID.g15025449; GSPDB:GN00166 A; Experimental source: Clostridium acetobutylicum ATCC824 C; Genecics: A; Genecics: Best Local Similarity A; Best Local Similarity A; Doury Match A; Best Local Similarity A; Genecics: Best Local Similarity A; Genecics: Best Local Similarity A; Genecics Best Local Similarity A; Genecics Best Local Similarity	RESULT 11 T15287 probable secreted proteinase - Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Accession: T32837 A:Resule: pre-liminary: D: Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. A:Resule: pre-liminary: translated from GB/EMBL/DDBJ A:Resule: pre-liminary: translated from GB/EMBL/DDBJ A:Resule: pre-liminary: translated from GB/EMBL/DDBJ A:Resule: pre-liminary: translated from GB/EMBL/DDBJ A:Resule: pre-liminary: translated from GB/EMBL/DDBJ A:Resule: pre-liminary: translated from GB/EMBL/DDBJ A:Resule: pre-liminary: pre-liminary: properties from GB/EMBL/DDBJ A:Resule: pre-liminary: properties from GB/EMBL/DDBJ A:Resule: pre-liminary: properties from GB/EMBL/DDBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GB/EMBL/GBJ A:Resule: pre-liminary: properties from GBJ A:Resule: properties from GBJ A:Resule: properties from GBJ A:Resule: properties from GBJ A:Resule: properties from GBJ A:Resule: properties from GBJ A:Resule: properties from GBJ A:Resule: properties from GBJ A:Resule: properties from GBJ A:Resule: properties from GBJ A:Resule: properties from GBJ A:Resule: properties from GBJ A:Resule

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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA, Res. 8, 205-213, 2001.
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak
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periplasmic proteinase XF2241 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species Xylella fastidiosa
C;Species Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: A8281
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MID1:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Status: preliminary
A;Note: for a complete list of authors see reference number A59328 below
A;Status: preliminary
A;Residuae: L-Status: A825184
A;Status: Dreliminary
A;Residuae: L-Status: A82004037; GB:AB0003849; NID:99107394; PIDN:AAF85040.1; GSPDB:GNO01
A;Streencental source: strain 9a5c
R;Simpson, A.JG: Reinand, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S: Bueno, M.R.P.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.S.; Franca, S.C.; Franco, M.C.; Forbur
Submitted to GenBank, June 2000
A;Authors: Ferraira, W.C.A.; Ferro, J.A.; Ferro, J.P.; Krieger, J.B.; Kurames, B.E.; Laigr
Chado, M.A.; Madeira, A.M.B.N.; Matsukuma, A.Y.; Manck, C.F.M.; Miraca, B.E.; Laigr
Chado, M.A.; Madeira, A.M.B.N.; Matsukuma, A.Y.; Manck, C.; M.; Miraca, B.C.; Palmieri, D. A;Authors: da Silva, A.G. de Silva, F.R.; da Silva, A.M.; Silva JT., W.A.; da Silva, A;Arthors: da Silva, A.G. da Silva, P.R.; da Silva, A.M.; Silva JT., W.A.; da Silva, A;Acherica.
A;Reference number: A93928
A;Cornente: annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NSRIHT-RCFGLLAITLPLAACGAQHNNSPTPTAPSTPIVTP---STTPAPQLVAGLPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQLVDQVGPGVVNIETVITRKKVGKRRGIPLDNDIPEFFRRFFGPDFQMPNQPRGGDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.0%; Score 341.5; DB 2; Length 514;
llarity 31.6%; Pred. No. 6.1e-13;
Conservative 55; Mismatches 128; Indels 83.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: Helicobacter serine proteinase
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Serine proteinase [imported] - Nostoc sp. (strain PCC 7120)
C,Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120
C,Note: Nostoc sp. strain PCC 7120
C,Note: Nostoc sp. strain PCC 7120
C,Accession: AB2057
R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. NA Res. B, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A,Reference number: AB1807; MUID:21595285; PMID:11759840
A,Status: preliminary
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                          C; Superfamily: Escherichia coli trypsin-like proteinase degs; GLGF domain homology; tryps
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                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                A)Residues: 11429 KKUR>
A;Cross-references: GB:BA000019; PIDN:BAB72659.1; PID:g17130047; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 VDRDKGVI,VVRVI.PINSPAARAGI.RAGDVI.QKI.NGQAVTDASNVQRAVENAQVGGQI.QI.EL 406
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A,Residues: 1-416 <KUR>
A,Residues: 1-6 <KUR>
A,Cross-references: GB:BA000019; PIDN:BAB73707.1; PID:g17131098; GSPDB:GN00179
A,Experimental source: strain PCC 7120
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 TGIISATGRT----SNQIGAPDKRVEYIQTDAAINPGNSGGPLINYRGEVIGWNTAIIQG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVN- 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 PGRVVALGQTVQASDSLTGAEETINGLIQPDAAIQPGDSGGPVVNGLGQVVGNNTAASDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                       71;
                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 429;
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                                                                                                                                                                                                                                                                                                                                                                  ; Score 335.5; DB 2;
; Pred. No. 1.1e-12;
59; Mismatches 137;
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Local Similarity 29.2%;
tes 110; Conservative 5
                                                       A,Accession: AD1894
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                             A;Gene: alr0702
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Best Local S.
Matches 110
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Gaps

18.4%; Score 331; DB 2; Length 416; ilarity 31.5%; Pred. No. 2e-12; Conservative 57; Mismatches 115; Indels 28;

Query Match Best Local Similarity Matches 92; Conserva

serine proteinase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD1894

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361 DIIQSINNQSVTTVEQVQKIVENSQIGQPLQIQIE-RNGQTTQVNVSPAPLP 411	qq
 302 DVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRIGNVTLAEGP 353	ò
 301 IQGKVDHPYLGVQMATLTPQVKERINERFGDRINITADRGVLLVRIVPGSPAANAGLRPG 360	Д
 255 SGGGSPTVHIG-PTAFLGLGVVDNNGNGARVQRVVGSAPAASLGISTG 301	λö
 245 DYLQTDAAINPGNSGGPLLNARGQVIGMNTAIIQGAQGLGFAIPINTVQKVSQELI 300	qq
 195 GLIQFDAAIQPGDSGEVVNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGGIR 254	Š
 GLININS VTSC	qq
 137 GLPSAAIGGGVAVGEPVVAMGNSGQQGTPRAVPGRVVALGQTVQASDSLTGAEBTLN 194	Š
 133 GSGSGFIISSSGQILTNAHVVDGADEVTV-TLKDGRSFDGKVLGEDPVTDVAVIQI-NAN 190	Dp
 77 GAGTGIVIDPNGVVITNNHVIAGATDINAFSVGSGQIYGVDVVGYDRTQDVAVLQLRGAG 136	ò

Search completed: June 30, 2004, 16:53:57 Job time: 13.2781 secs

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Page 1

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model	1: June 30, 2004, 16:42:21; Search time 5.77978 Seconds (without alignments) 3198.204 Million cell updates/sec
	OM protein	Run on:

US-09-597-796C-4
1802
1 MSNSRRRSLRWSWLLSVLAA.....QTXSGGTRTGNVTLAEGPPA 355

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PRTC_STRGR ELS_BOVIN	Y747 MYCTU YI40 MYCTU	PRTB_STRGR	WA2Z MYCTU	Y278_MYCTU	FIB1 ADEG1	OMPA_RICCN	YQ34 MYCTU	PGCA_BOVIN
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ALIGNMENTS

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	YVTA OR YVTB OR BSU33000.
S C	Bacillus Subtilis. Bactoria: Rirmicutos: Racillalos: Racillacoao: Racillus.
88	I_TaxID=1423;
NN DD	[1] Sentence reom n a
	STRAIN=168;
	MEDLINE=20158875; PubMed=10692364;
8 E	Noone D., Howell A., Devine K.M.; "Froression of vkdå, encoding a Bacillus subtilis homologue of HtrA,
	J. Bacteriol. 182:1592-1599(2000).
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Z.	Microbiology 143:3305-3308(1997).
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RA.	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
R.A	Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA	Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA	Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Z S	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel K.A.,
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\$ &	Bincian N.D., Billing V. Fuma S. Gallizzi A., Galleron N., Fritz C. Fuitta M. Fuitta Y., Fuma S., Gallizzi A., Galleron N.,
Æ	Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA	Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Z G	Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
4 4 4 4	UOILB D., Nafaulata D., Nabadiata I., Nigeti-bianchair H., Nieti C., Kobavashi V. Koeffer D. Konindstein G., Krodh S., Kumano M.
Z.	Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA.	Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA	Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
8 4 4	NOODE D., O'RELLLY M., Ogawa K., Oglwara A., Oudega B., Fark S.R., Darro V. Dohl T.M. Portetelle D. Porwollik S., Prescott A.M.,
Z.	Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA:	A Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
R G	Sato T., Scanlan E., Schleich S., Schroeter R., Scottone F.,
¥ 6	Seriguani U., Serowska A., Seru B.C., Seriot F., Shiil B.C., Solice E., Seriot B. Takemari K.
§ §	Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA	Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

151 244 268

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NHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGE
                                      186 NHVVEGANKLTV-TLYNGETETAKLVGSDTITDLAVLEISGKNVKKVASFGDSSQLRTGE
                                                                                              245 KVIAIGNPLGQQFSGTVTQGIISGLNRTIDV-DTTQGTVEM--NVLQTDAAINPGNSGGP
                                                                                                                                          212 VVNGLGQVVGNNTAASDNFQLSQGG---QGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTA
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                                                                                                                                                                                                       FLGLGVVDNN-------GNGARVQRVVGSAPAASLGISTGDVITAVDGA
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STRAIN-KI2 /, MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli, and
Escherichia coli (157:H7.
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae, Escherichia.
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Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                   311 PINSATAMADAL-NGHHPGDVISVNWQTKSGGTRTGNVTLAE 351
                                                                                                                                                                                                                                                                                                411 DVESSADIRQILYKDLKVGDKTTIQ-VLRKGKTKTLNATLTK 451
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01-FEB-1995 (Rel: 31, Last sequence update)
28-FEB-2003 (Rel: 41, Last annotation update)
Procease degS precursor (EC 3.4.21.-)
DEGS OR HHOB OR HTRH OR B3235 OR Z4594 OR ECS4108.
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STRAIN=K12 / W110;
MEDLINE=96165272; PubMed=8576051;
Waller P.R., Sauer R.T.;
"Characterization of degQ and degS,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homologs of the DegP protease.";
J. Bacteriol. 178:1146-1153(1996)
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STRAIN=K12 / W3110;
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Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Waiters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H., Danchin A., "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A----MVAQVAPQVVNI-NTKLGYNNAV-------GAGTGIVI---DPNGVVLTN
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77551045A865A5CD CRC64;
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EXTRACELLULAR (POTENTIAL).
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EMBL; 239341; CAB07968.1; ALT FRAME.
EMBL; 23941; CAB07968.1; ALT FRAME.
EMBL; 299120; CAB16220.1; ALT FRAME.
EMBL; 299120; CAB16220.1; ALT FRAME.
Subtilist; BG14155; YvtA.
INTERPOOR DEROUHOUS, PDZ.
INTERPOOR DEROUHOUS, PDDLINGSPOOR DEROUHOUS, PEDTIGASE S1.
INTERPOOR DEROUHOUS, PEDTIGASE S1.
PÉAM; PF00089; trypsin; 1.
PÉAM; PR0089; trypsin; 1.
PÉAM; PR0089; trypsin; 1.
PRINTY; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                        MEDLINE=20576168; PubMed=11133960;
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FRANSCRIPTIONAL REGULATION.
                                                                              Nature 390:249-256(1997).
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Enterobacteriaceae; Escherichia NCBI TaxID=562;
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; Pred. No. 1.1e-11;
47; Mismatches 135; Indels 66; Gaps 13;
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                                                                                                                                                                  PRELIMINARY SEQUENCE OF 82-355 FROM N.A.
MEDLINE=88105815; PubMed=332223;
Vogel R.F., Entian K.-D., Mecke D.;
"Cloning and sequence of the mch structural gene of Escherichia colicolang for malake dehydrogenase.";
Arch. Microbiol. 149:36-42(1987).
                                                                                                                                                                                                                                                                                                          Bazan J.F., Fletterick R.J.;
"Structural and catalytic models of trypsin-like viral proteases.";
Semin. Virol. 1:311-322(1990).
-!- SUBCELGULAR LOCATION: Periplasmic (Potential).
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
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307 V -> E (IN REF. 6).
37581 MW; D091B4D65E8FEICC CRC64;
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EMBL; U32495; AAC44006.1; ---
EMBL; U18997; AAC44006.1; ---
EMBL; AE000402; AAC76267.1; ---
EMBL; AE005551; AAC5833.1; ---
EMBL; AP002564; BAB37531.1; ---
EMBL; AP02564; BAB37531.1; ---
EMBL; AP02564; BAB37531.1; ---
EMBL; AP02564; BAB37531.1; ---
EMBL; AP02564; BAB37531.1; ---
EMBL; AP002564; BAB37531.1; ---
EMBL; AP002564; BAB37531.1; ---
EMBCPS; SO1.275; ---
ECGGHG; EG11652; hob.
InterPro; IPR001040; Cys_Ser_trypsin.
InterPro; IPR001264; Peptidase_S1C.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00894; PRDZ; 1.
PRINTS; PR00894; PRDZ; 1.
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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Hydrolase; Serine protease;
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Best Local Similarity 30.7<sup>3</sup>
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                                                                                                                                                                                                                                             175 ALGOTV-QASDSLTGAEETLN----GLIQFDAALQPGDSGGPVVNGLGQVVGMNTAASD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 KSNDGETPEGIGFAIPFQLATKIMDKLIRDGRVIRGYIGIGGR----ELAPLHAQGGGI- 276
62 ----YNRGLNITNSHNQLEIRTLGSGVIMDORGYIITNKHVINDADQI-IVALQDGRVFEA 116
                                                                                                                                                                                                                                                                                                                                                                                           229 --NFQ1SQGGQGFAIP-----IGOAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV 275
                                                                                                        DVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVA--VGEPVVAMGNSGGQGGTPRAVPGRVV 174
                                                                                                                                                                                                                                                                                                                163 NLGOTITQGIISATG-RIGLNPTGRONFLOTDASINHGNSGGALVNSLGELMGINTLSFD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISV 333
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                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=K12 / MG1655;

MEDILINE=97426617; PubMed=9278503;

MEDILINE=97426617; PubMed=9278503;

A Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., A Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., A Mau B., Shao Y.;

A Mau B., Shao Y.;

The complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).

-! FUNCTION: PROTEASE WITH A SHARED SPECIFICITY WITH DEGP/DEGP.

-! SUBCELLULAR LOCATION: Periplasmic.

-! SUBCELLULAR LOCATION: Periplasmic.

-! SIMILARITY: Contains 2 PDZ/DHR domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / W3110;
Bass S., Gu Q., Goddard A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A., AND SEQUENCE OF 28-32.
STRAIN=X12 / W3110;
MEDLINE=96165272; Pubmed=8576051;
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BY SIMILARITY
PROTEASE DO.
PDZ 1.
PDZ 2.
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29.1%;
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Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                Nature 413:852-856(2001)
                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 VGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ATSGIVSALGR-----SGLNLEGLENFIQTDASINRGNSGGALLNLNGELIGINT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |----LAPGGGSVGIGFAIPSNMARTLAQQLIDFGEIKRG------LLGIKG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------KLGYNNAV-----GAGTGIVIDPN-GVVLTNNHVIAGATDINAFS 107
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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PDZ 2.
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
PER, JC6051; JC6051.

MENOPS; SOL1224;

SWISS-2DPAGE; P39099; COLI.

RECOGENE; EG12612; degQ.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001940; Peptidase_S1.

Pfam; PF00089; trypsin; 1.

R Pfam; PF00089; trypsin; 1.

R PRINTS; PR0084; PROTEASES2C.

R PROSITE; PS50106; PDZ; 2.

R PROSITE; PS50106; PDZ; 2.

R HYGTOLASE; SETINE protease; Periplasmic; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.1%; Score 326; DB 1; Length 455; 30.4%; Pred. No. 1.9e-11; Indels iive 61; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          6A090F93AC021C83 CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Proctease do precursor (EC 3.4.21.-).
DEGP OR HTRA OR PTD OR STM0209.
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258 349 PDD
355 447 PDZ
109 109 CHP
139 139 CHP
214 CHB
214 CHB
455 AA; 47205 MW; 6
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Matches 119; Conservative
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SEQUENCE FROM N.A.
STRAIN=C5;
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P26982;
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DR InterPro; IPR00124; Ppg1dase_S1.

DR InterPro; IPR001254; Ppg1dase_S1.

DR PEAM; PF00089; Priypsin; 1.

DR PEAM; PF00089; Priypsin; 1.

DR PEAM; PR00081; PROTEASES2C.

RMART; SM00228; PDZ; 2.

R PROSITS; PSG106; PDZ; 2.

R PROSITS; PSG106; PDZ; 2.

R Complète protease; Heat shock; Periplasmic; Repeat; Signal; T SIGNAL.

T SIGNAL.

T SIGNAL.
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                                                                                                                                                                                                                                                                                                    STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCTCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtiety L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
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-!- SUBCELLULAR LOCATION: Periplasmic.
MEDLINE-91251770; PubMed=1645840;
Johnson K., Charles I., Dougan G., Pickard D., O'Gaora P., Costa Ali T., Miller I., Hormaeche C.;
"The role of a stress-response protein in Salmonella typhimurium virulence.";
Mol. Microbiol. 5:401-407(1991).
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CHARGE RELAY SYSTEM (POTENTIAL).
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- INDUCTION: By hear shock.
-i- SIMILARITY: Belongs to peptidase family S2C.
-i- SIMILARITY: Contains 2 PDZ/DHR domains.
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Query Match
Best Local S:
Matches 89
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 236
                                                                                              SGGPVVNGLGQVVGMNTA--ASDNPQLSQGGGFAIP-----IGQAMAIAGQIRSGGGS 259
                                                                                                                                                  260 PTVHIGPTAFLGLGVVDNNGN------GARVQRVVGSAPAASLGISTGDVITA 306
                                                                                                                                                                            ------ELGIMGTELNSELAKAMKVDAQRGAFVSQVMPNSSAAKAGIKAGDVITS 339
                                                                                                              SGGALVNLNGELIGINTAILAPDGGNI---GIGFAIPSNMVKNLTSQMVEYGQVKRG---
                                         VGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAE-ETLNGLIQFDAAIQPGD
                                                                  VGDYTVAIGNPFGLGET--VTSGIVSALGR----SGLNVENYENFIQTDAAINRGN
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CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
B16B677991C88707 CRC64;
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"Molecular characterization of a stress-inducible gene from
"Lactobacillus helveticus.";
J. Bacteriol. 180:6143-6153(1998).
-!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-!- SIMILARITY: Belongs to peptidase family $2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                       307 VDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAE 351
                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes; Lactobacillales, Lactobacillaceae,
Lactobacillus.
NCBI_TaxID=1587;
                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-PEB-2003 (Rel. 41, Last amnotation update)
Serine protease do-like htrA (EC 3.4.21.-).
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InterPro; IPR001478; PDZ_
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PP00595; PDZ; 1.
Pfam; PP00899; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
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150
180
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413 AA;
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SEQUENCE
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                                                                                                                                                                                             119 SSKNGKLETYSEGSGVVYMKSNGKGYIVTNNHVISGSDAVQVL-LANGKTVNAKVVGKDS
                                                                                                                                                                                                                                                                                                                                               67 NTKLGYNNAVGAGTGIVI---DPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDV
                                                                                                                                                                                                                                                                                                    TODVAVLOLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 ASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNT--AASDNFQLSQGGQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 TS---SGNQQT---VIQTDAAINPGNSGGALVNSAGQVIGINSMKLAQSSDGTSVEGMAF
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STRAIN-KI2 / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Rilet M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=94261430; PubMed=8202364;

MEDLINE=94261430; PubMed=87. Ishihama A.;

Fujita N., Mori H., Yura T., Ishihama A.;

"Systematic sequencing of the Escherichia coli genome: analysis of the 2.4-4.1 min (110, 917-193, 643 bp) region.";

Nucleic Acids Res. 22:1637-1639(1994).
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P09376; P15724;
P014MA-1999 (Rel. 10, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
DEGP OR HITA OR PTD OR B0161 OR Z0173 OR ECS0165.
BECHETICHIA COli, and
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae, Escherichia.
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                                                                               24;
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Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung Schramm S., Komp C., Kurdi O Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
       Length 413;
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Science 277:1453-1474(1997)
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                                                                               121; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 SAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISV : | | | | | | | | ::|
17.8%; Score 321; DB 1; 31.3%; Pred. No. 3.2e-11; ive 50; Mismatches 121;
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                                                                                   89; Conservative
                                               Similarity
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88 -GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPS--AAIG 144
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ECOGENE; EGIO463; degP.
ENCEPTO: IPR001903; Cys.Ser.trypsin.
INCEPTO: IPR001478; PDZ.
INTERPO: IPR001949; Peptidase_S1.
INCEPTO: IPR001940; Peptidase_S1.
PEAM; PP00595; PDZ; Z.
PEAM; PP00595; PDZ; Z.
PEAM; PR00595; PDZ; Z.
PEAM; PR00595; PDZ; Z.
                                                                                                                                                                                                                                                   Complete proteome; 3D-structure. SIGNAL 1 26
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Matches 112, Conservative
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MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
Mayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
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MEDLINE=90202693; PubMed=2180903;
Lipinska B., Zylicz M., Georgopoulos C.,
"The HrrA (DegP) protein, essential for Escherichia coli survival at high temperatures, is an endopeptidase.";
J. Bacteriol. 172:1791-1797(1990).
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SEQUENCE OF 1-16 FROM N.A.
SEQUENCE OF 1-16 FROM N.A.
MEDLINE=90207273; PubMed=2157212;
Wurgler S.M., Richardson C.C.;
Wurgler S.M., Richardson C.C.;
"Structure and regulation of the gene for dGTP triphosphohydrolase from Escherichia coli.";
from Escherichia coli.";
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                                                      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Abodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blatthar F.R., Lin J., Yen G., Schwartz D.C., "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTITY OF HTRA AND PROTEASE DO.

MEDLINE-21222240, PubMed-2025268,
Seol J.H., Woo S.K., Jung E.M., Yoo S.J., Lee C.S., Kim K.J.,
Tanaka K., Ichihara A., Ha D.B., Chung C.H.;
Protecase Do is essential for survival of Escherichia coli at high
temperatures: its identity with the htra gene product.";
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; Pubmed=11206551;
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90323597; PubMed=2165018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteome projects.";
J. Mol. Biol. 278:599-608(1998).
                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-50 FROM N.A. STRAIN=K12;
                                                                                                                                                        Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 89:13-18(1990).
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STRAIN=K12 / W311(
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E -> Q (IN REF. 7).
A -> G (IN REF. 1).
STITING -> RHLPVNAVISINPFLKTGRGSPYNL (IN REF. 1).
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29.8%; Pred. No. 5.7e-11;
ive 51; Mismatches 108; Indels 105; Gaps
INVOLVED IN THE DEGRADATION OF DAMAGED PROTEINS. IT CAN DEGRADES ICIA, ADA, CASEIN AND GLOBIN. SHARED SPECIFICITY WITH DEGQ. SUBGULT: Multimeric. SUBCELLULAR LOCATION: Periplasmic.
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PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Heat shock; Periplasmic; Repeat; Signal;
                                                                    -!- SUBUNIT: MULTIMEALY.
-!- SUBCELLUIAR LOCATION: Periplasmic.
-!- INDUCTION: By heat shock.
-!- ALSCELLANBOUS: HTRA IS INDISPENSABLE FOR BACTERIAL SURVIVAL AT TEMPERATURES ABOVE 42 DEGREES CELSIUS.
TEMPERATURES ABOVE to peptidase family $2C.
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408 AA;
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Q8YG32;
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                                                                                                                                                                                                                                          GGGSPTVHIGPTAFLGLGVVDNNGN-------GARVQRVVGSAPAASLGISTGD 302
                                                                                                                                                                                                                                                                                  334
Meissenbach J., Wincker P., Manger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis Lil403."
Genome Res. 11:731-753(2001).
- FUNCTION: DEGRADES ABNORMAL EXPORTED PROTEINS. NEEDED FOR THE PRO-
PEPTIDE PROCESSING OF A NATURAL PRO-PROTEIN AND FOR MATURATION OF
A NATIVE PROTEIN. RESPONSIBLE FOR THE HOUSEKEEPING OF EXPORTED
                                                                                        QPGDSGGPVVNGLGQVVGMNTA--ASDNFQLSQGGQGFAIP-----IGQAMAIAGQIRS
                                                              GGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAB-ETLNGLIQFDAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmfoutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=IL1403;
MEDLINE=20177820; PubMed=10712686;
MEDLINE=20177820; PubMed=10712686;
Poquet I., Saint V., Seznec E., Simoes N., Bolotin A., Gruss A.;
"Htra unique surface housekeeping protease in Lactococcus lactis and is required for natural protein processing.";
Mol. Microbiol. 35:1042-1051(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Membrane-bound (Probable). SIMILARITY: Belongs to peptidase family S2C. SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine protease do-like htrA (EC 3.4.21.-) (HtrAL1).
HTRA OR LL2136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 AA.
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InterPro; IPR001478; PDZ.
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MEDLINE=21235186; PubMed=11337471;
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Peptidase_S1C.
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335 VITSLNGKPISSFAAL 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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InterPro; IPR001940;
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MEROPS; S01.273; -.
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Q9LA06;
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HTRA_LACLA
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SEQUENCE STRAIN=16M / ATCC 23456 / Biotype 1;

MEDIINE=200020109; bubMed=1175668x R.J., Patra G., Mujer C., Los T.,

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

Albolonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Aselkov E., Bizer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Anselkorn R., Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

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Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SMO0228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
Hydrolase; Serine protease; Transmembrane; Complete proteome.
TRANSMEM 6 26
CATALYTIC.
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Brucellaceae; Brucella.
NCBI_TaxID=29459;
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
DEGP OR HTRA OR BMEI1330.
Brucella melitensis.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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PDZ 2.
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SPECIES=B.suis; STRAIN=1330 / Biovar 1;
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EMBL, AE014588, AAN29540.1, --
PIR, 140060, 140060.
TIGR; BR0611, --
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Matches 126; Conservative
                                                 Brucellaceae; Brucella.
                                                                            NCBI_TaxID=29461, 235;
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 306; DB 1; Length 513;
; Pred. No. 2.7e-10;
43; Mismatches 142; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE
CATALYTIC.
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CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
                                                               EMBL, AE009571; AAL52511.1; -.
PIR; AD3418; AD3418.
InterPro; IPR009003; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
InterPro; IPR001940; Peptidase_S1C.
InterPro; IPR001950; Irypain; 1.
PRINTG; PR001981; PR0TEASES2C.
SMART; SM00228; PSZ. 2.
IPROSTITE; PSS0106; PDZ; 2.
IPROSTITE; PSS0106; PDZ; 2.
IPROSTITE; PSS0106; PDZ; 2.
IPROSTITE; PSS0106; PDZ; 2.
IPROSTITE; PSS0106; PDZ; 2.
IPROSTITE; PSS0106; PDZ; 2.
IPROSTITE; PSS0106; PDZ; 2.
IPROSTITE; PSS0106; PDZ; 2.
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IPROSTITE; PSS0106; PDZ; 2.
IPROSTITE; PSS0106; PDZ; 2.
IPROSTITE; PSS0106; PDZ; 2.
IPROSTITE; PSS0106; PDZ; 3.
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444597;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
40-MAY-2003 (Rel. 41, Last annotation update)
41-May annotation update)
42-MAY-2003 (Rel. 41, Last annotation update)
43-MAY-2003 (Rel. 41, Last annotation update)
44-MAY-2003 (Rel. 41, Last annotation update)
45-MAY-2003 (Rel. 41, Last annotation update)
46-MAY-2003 (Rel. 41, Last annotation update)
47-MAY-2003 (Rel. 41, Last annotation update)
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entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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43; Mismatches 142; Indels 136;
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R InterPro; IPR001254; PDZ.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR00199; 2.
R Pfam; PR0089; trypsin; 1.
R PRINTS; PR0089; trypsin; 1.
R SMART; PR00228; PDZ; 2.
Hydrolase; PDZ; 2.
Hydrolase; Serine protease; Periplasmic; Repeat; Signal; Complete protease; Potential.
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A. Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,
A. Tanaka S., Vandenbol M., Vannier F., Vassarotti A.,
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  ----GYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAF
                                                                                                217 NPFGLGGT--VTSGIVSARGRDIGAG------PYDDFIQIDAAVNKGNSGGPAFDLSG
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NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable serine protease do-like htrA (EC 3.4.21.-).
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Anovel two-component regulatory system in Bacillus subtilis for the Navel two-component regulatory system in Bacillus subtilis for the Stream in Secretion stress.";

Mol. Microbiol. 41:1159-1172(2001).

L. FUNCTION: May be involved in processing, maturation, or secretion of extracellular enzymes.

C. INDUCTION: Transcription is cass dependent. Induced by heat shock during exponential growth and by heterologous amylases at the transition phase of the growth cycle. Negatively regulates its own transition phase of the growth and during heat shock.

C. INTSCLIANGEOUS: Inactivation results in compensating overexpression of ytvh, especially during stress conditions.

C. INTSCLIANGEOUS: Inactivation results in compensating overexpression of ytvh, especially during stress conditions.

C. INTSCLIANGEOUS: INDUCTION: DESCRIPTIONS.

C. INTSCLIANGEOUS: INACTIVATION STRESS CONDITIONS.

C. INTSCLIANGEOUS: INACTIVATION PROPERTY COMPANIENTY: Contains I PDZ/PHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch)
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MEDINE=2055168; PubMed=11133960;
MEDINE=2055168; PubMed=11133960;
MOOME D., Howell A., Collery R., Devine K.M.;
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MEDINE=21439741; PubMed=11555295;
Hyyrylaeinen H.-L., Bolhuis A., Darmon E., Muukkonen L., Koski P.,
Vitikainen M., Sarvas M., Pragai Z., Bron S., van Dijl J.M.,
Kontinen V.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease; Heat shock; Transmembrane;
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POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AJ002571; CAA05570.1; -. FMBL, A29910; CAB13147.1; -. PIR, A29910; CAB13147.1; -. PIR, A29643; A69643. A69643. A69643. A69643. A69643. A69643. A69643. A69643. A69643. A69643. A17.1; -. MEROPS, SOL.273; -. InterPro; IPR001479; PDZ. InterPro; IPR001479; PDZ. InterPro; IPR001284; Peptidase_S1. InterPro; IPR0015940; Peptidase_S1C. Pfam; PF00595; PDZ, 1. Pfam; PF00699; trypsin; 1. Pfam; PR001894; PROTEASESCC. SWART; SMO0228; PDZ, 1. PROSITE; PS50106; PDZ, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Protease; Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSCRIPTIONAL REGULATION.
                                                                                                                                                              TRANSCRIPTIONAL REGULATION.
                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTIONAL REGULATION.
                                                                                                                      Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44
67
108
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                                                                                                                           212
                                                                                                                                                                                                        HVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG--GGVAVGEP 152
                                                                                                                                                                        HVVEGASSLKV-SLYDGTEVTAKLVGSDSLTDLAVLQISDDHVTKVANFGDSSDLRTGET 237
                                                                                                                                                                                                                                     VNGLGQVVGNNT---AASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFL 270
                                                                                                                                                                                                                                                       LNTDGKIVGINSMKISEDDVE----GIGPALPSNDVKPIAEELLSKGQIERPYIG-VSML 349
                                                                                                                                                                                                                                                                            GLGVVDNN-------GNGARVQRVVGSAPASLGISTGDVITAVDGAPINSATA 317
                                                                                                                                                                                                                                                                                         94
                                                                                                               --VGAGTGIVI-DPNG--VVLTNN
                                                                                                                                                                                              VVAMGNSGGOGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Periplasmic (Potential).
-1- SUMILARITY: SEBNS TO BE A INTERMEDIATE FORMS BETWEEN E.COLI HTRA
-1- (PROTEASE DO) AND HHOA.
-1- SIMILARITY: Belongs to peptidase family $2C.
-1- SIMILARITY: Contains 2 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAINER / KW20 / ATCC 51907;

MEDLINE=5350630; PubMed=754800;

MEDLINE=5350630; Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Rine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Venter J.C.,
                                                                                            45;
         PDZ.
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                       Score 295.5; DB 1; Length 449; Pred. No. 8.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Probable periplasmic serine protease do/hhoA-like precursor (EC 3.4.21.-).
                                                                                8.9e-10;
thes 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                          53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            466 AA.
  POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                              53 SAMVAQVAPQVVNINTKLGYNNA--
                                                 47713 MW;
                                                                                                                                                                                                                                                                                                                    MADAL-NGHHPGDVISV 333
                                                                                                                                                                                                                                                                                                                                        LRNILYKDAKIGDTVEV 426
                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
                                                                      16.4%;
                                                                               29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
                                                                    Query Match
Best Local Similarity 29.3
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
152
437
179
209
290
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(Rel. 32,
(Rel. 41,
                                                449 AA;
 209
209
209
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01-NOV-1995
28-FEB-2003
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DOMAIN
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ACT SITE
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 GKAKVDSRSPFLDDIPEEFKFFFGDRFAEQFGGRGESKRNFRGLGSGVIINASKGYVLTN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 NHVIDGADKITV-QLQDGREFKAKLVGKDEQSDIALVQLEKPSNLTEIKFADSDKLRVGD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 PVVNGLGQVVGMNTAASDNFQLSQGQQ--FAIFIGQAMAIA-----GQIRSGGGSPTV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 HIGPTAFLGLGVVDNNGN------GARVQRVVGSAPAASLGISTGDVITAVDGAP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 NHVIAGAIDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSA--AIGGGVAVGE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 VLAAVGLGLATAP-----AQAAPPALSQDRFADFPALPLDPSAMVAQVAPOVVNINTK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VINSIALGESVLSTSFVAHVAQATLPSFVSEQNSLAP-----MLEKVQPAVVTLSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GVNLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 ALVNLNGELIGINTAI---ISPSGGNAGIAFAIPSNQASNLVQQILEFGQVRRG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEE-TLNGLIQFDAAIQPGDSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 FTVAIGNPFGLGQT--VTSGIVSALGRS-----TGSDSGTYENYIQTDAAVNRGNSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
PROBABLE PERIPLASMIC SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 295; DB 1; Length 46
Pred. No. 9.9e-10;
54; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSS0106; PD2, 2.
Hydrolase; Serine protease; Periplasmic; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2001 (Rel. 41, Last amnotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ED050A00047B5851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DO/HHOA-LIKE
                                                                                                                                                                                                                                                    InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ_
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 2.
Pfam; PF00089; irypsin; 1.
PRINTS; PR00834; iryDsin; 1.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INSATAMADALNGHHPGDVISVNW 335
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28.1%;
                                                                                                                                                              EMBL; U32805; AAC22906.1; -.
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Best Local Similarity 28.15
Matches (108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
458
120
150
                                                                                                                                                                                       PIR; A64113; A64113.
MEROPS; S01.274; -.
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367
120
150
226
466 AA;
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30-MAY-2000
30-MAY-2000
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SEQUENCE
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12;

Gaps

38;

GTGIVIDPNGVVLTNNHVIAGATDINAFSV--GSGQTYGVDVVGYDRTQDVAVLQL--RG

39; Mismatches 117; Indels

97; Conservative

Matches

C ター・サーンのハー / ハローハコーロコ

79

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304 ITAVDGAPINSATAMADALNGHHPGDVISVN-WQTKSGGTRIGNVTLAEGP 353

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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
LL -> PV (IN REF. 1).
LL -> PV (IN REF. 1).
EDPENHUNDAVSPAVUSVQARENUSDESNETEDEGGRGF
RDLEDHPLRRFREFAPRENDRADRWRDRGPRGEGRLRP
RAGGGGFFTTEDGYLVTNHVSDGSA. -> AVSPWSTPF
RRRSSPSACRHVNASATMKATSPSISAAAGSRTCRKTIRGG
VSSANSLRVKMTVPIVGATAAVRVAKVYSGRKAPASSSP
                                                                                                                                                                                                                                                                            STRAIN=1021;
XM PEDLINR=2136507; PubMed=11481430;
A Gapela D., Barloy-Hubler F., Goury J., Bothe G., Ampe F., Batut J.,
A Gapela D., Barloy-Hubler F., Goury J., Eddieu E., Dreano S., Gloux S.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Godrie T., Goffeau A., Pubhler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
Renard C., Thebault P., Vandenbol M., Weidner S.,
I "Analysis of the chromosome sequence of the legume symbiont
XT "Analysis of the chromosome sequence of the legume symbiont
The Proc. Natl. Acad. Sci. U.S.A. 98:3877-3882 (2001).
I- SUBCELLULAR LOCATION: Periplasmic (Potential).
I- SUBCELLULAR LOCATION: Periplasmic (Potential).
C -- SIMILARITY: Belongs to peptidase family $2C.
I- SIMILARITY: Contains 2 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTVTSSPTTTSSPTART (IN REF. 1).
KSADDVLKVINNAKKDGRSKALFQIBAQEGSRFVALPITQG
-> NRQTTFSR (IN REF. 1).
                                                                                               SEQUENCE FROM N.A.
STRAIN=1021;
MEDIINE=96146524; PubWed=8550509;
Glazebrook J., Ichige A., Walker G.C.;
Genetic analysis of Rhizobium meliloti bacA-phoA fusion results in identification of degP: two loci required for symbiosis are closely linked to degP:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
CATALYTIC.
DEGPI OR DEGP OR RO1021 OR SMC02365.
Rhizobium mellioti (Sinorhizobium mellioti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS50106, PDZ, 2.
Hydrolase, Serine protease, Periplasmic, Repeat, Signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D7E82BB9981EA23C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U31512; AAG43669.1; ALT_INIT.
EMBL; AL591785; CAC45593.1; -.
MEROPS; S10.273; ..
INTERPRO; S10.273; ..
INTERPRO; IPRO01903; Cys_Cr_trypsin.
INTERPRO; IPRO0194; PDZ.
INTERPRO; IPRO01940; Peptidase_S1.
INTERPRO; IPRO01940; Peptidase_S1.
Ffam; PF00895; PDZ; 2.
PRAMT; PR00894; PRCTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                            J. Bacteriol, 178:745-752(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 AA; 53035 MW;
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286
286
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                                                                     NCBI_TaxID=382;
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DEGREEATHE STANDARD, PRT, 503 AA.

DEGREEATHE STANDARD, PRT, 503 AA.

DEGREEATHE STANDARD, PRT, 503 AA.

DEGREEATHE STANDARD, PRT, 503 AA.

DEGREEATHE STANDARD, PRT, 503 AA.

DEGREEATHE STANDARD, PRT, 503 AA.

DEGREEATHER, 14, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

NEW DEGREEATHER UPTO-1000 (Rel. 34, Last sequence update)

NEW DEGREEATHER UPTO-1000 (Rel. 34, Last sequence update)

NEW DEGREEATHER UPTO-1000 (Rel. 34, Last sequence update)

NEW DEGREEATHER UPDATED (Rel. 34, Last sequence update)

NEW DEGREEATHER UPDATED (Rel. 34, Last sequence update)

NEW DEGREEATHER UPDATED (Rel. 34, Last sequence update)

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NEW DEGREEATHER UPDATED (REL. 34, Last update)

NEW DEGREEATHER UPDATED (REL. 34, Last update)

NEW DEGREEATHER UPDATED (REL. 34, Last
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291; DB 1; Length 504; No. 1.8e-09;

Score Pred.

16.1%; 33.3%;

Query Match Best Local Similarity

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                                                                                                                                                                                            16;
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                                                                                                                                                                                                                                                                                                                                                       79 FSDFFSTPGFDQLPDQHPLKKFFQDFYNRDKPSNKSLQRSHRLRPIAFGSGFFISSDGYI 138
                                                                                                                                                                                                                                                                                                                                                                                                 LINNHVIAGAIDINAFSVGSGQTYGVDVVGYDRIQDVAVLQLRGAGGLPSAAIG--GGVA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 VTNNHVISDGTSY-AVVLDDGTELNAKLIGTÖPRTÖLAVLKVNEKRKFSYVDFGDDSKLR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 TAFLGLGVVDNNGNGARVQRV-----VG------SAPAASLGISTGDVITA 306
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                                                                                                                                                                                                                                                                                                                    90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 GGPTFDLNGKVVGVNTAL---FSPSGGNVGIAFAIPAATANEVVQQL-------
                                                                                                                                                                                                                                                                        GSSLWTTKAHANSVFSSLMQQQGFAD-----IVSQVKPAVVSVQVKKEWF
                                                                                                                                                                                                                                                                                                                    -----NAVGAGTGIVIDPNGVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGDWVVAIGNPFGLGGTVTA--GIVSARGR-----DIGTG---VYDDFIQIDAAVNRGNS
                                                                                                                                                                  27.7%; Pred. No. 2e-09;
tive 42; Mismatches 135; Indels 118; Gaps
                                                                                                                                                                                                                               22 GLGLATAPAQA---APPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLG-----
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022609; OSPIKRS;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protease Do-like 1, chloroplast precursor (EC 3.4.21.-).
Protease Do-like A7362795. OR K61012.18
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.
NCBL TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Columbia;
MEDLINE=20363099; PubMed=10907853;
Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=98175982; PubMed=9507020;
Itzhaki H., Naveh L., Lindahl M., Cook M., Adam Z.;
Itdentification and characterization of DegP, a serine protease associated with the luminal side of the thylakoid membrane.";
J. Biol. Chem. 273:7094-7098(1998).
PDZ 1.
PDZ 2.
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 VDGAPINSATAMADALNGHHPGDVISVN-WQTKSGGTRTGNVTLAEGP 353
                                                                                                                                                Score 290; DB 1; Length 503;
                                                                                                      6CD9F4743282AF9E CRC64;
                                                                                                         54114 MW;
                                                                                                                                              16.1%;
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466
143
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247
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STRAIN=cv. Columbia;
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STRAIN=cv. Columbia;
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    DOMAIN
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DEGI_ARATH
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DOT 022609,
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DT 16-0CT-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 SAFVVSTPKKLOTDELATVRLFQENTPSVVYITNLAVRODAFTLDVLEVPQGSGSFVWD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 AIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
Kieselbach T., Bystedt M., Schroeder W.P., Submitted (JUL-2000) to Swiss-Prot.
--- FUNCTION. Serine protease that is required at high temperature.
May be involved in the degradation of damaged proteins. In vivo, can degrade beta-casein.
--- ENZYME REGULATION: Inhibited by phenylmethylsulfonyl fluoride and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16. KOĞHIVTINYHVIRGASDLKV-TLADQTTFDAKVVGFDQDKDVAVLRIDAPKNKLRPIP-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 PNGVVLTNNHVIAGATDINAFSVGSGOTYGVDVVGYDRTODVAVLQLRGAGG----LPSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transit peptide; Chloroplast; Thylakoid. CHLOROPLAST (POTENTIAL).
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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
HSPPSKQLSNST -> SSTLFLHSPPSSHL (IN REF.
                                                                                                                                                  O-phenanthroline.
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V -> I (IN REF. 2).
V -> I (IN REF. 2).
G -> R (IN REF. 2).
IL -> HF (IN REF. 2).
L -> V (IN REF. 2).
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W, 1497BlAB3F5FF2A4 CRC64;
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                                                                                                                                                                                                                     -!- INDUCTION: By heat shock.
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DO-LIKE 1.
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PROTEASE DO-LIKE
SERINE PROTEASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001478; PDZ_
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 1.
Pfam; PF008091; PROTEASES2C.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; ÁF028642; AAC39436.1; -.
EMBL; ÁP000311; BAB02539.1; -.
EMBL; AP001302; BAB02539.1; JOINED.
MEXOPS; S01.279; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PSS0106; PD2; 1.
PYGCOLASE, Serine procease; Transit 7 103
TRANSIT 7 103
CHAIN 104 437 F DOMAIN 152 331 S DOMAIN 324 431
ACT SITE 171 171 C ACT SITE 280
CONFLICT 12 280
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                                                           324
                                                                                         302
                                                                                                         220 GVSADLLVGQKVFAIGNPFGLDHT--LTTGVISGLRREI--SSAATG--RPIQDVIQTDA 273
                               AIQPGDSGGPVVNGLGQVVGMNTAASDNFQLSQGGGFAIPIGQAMAIAGQIRSGGGSPT 261
                                                                                         262 VHIGPTAFLGLGV------VDNNG-NGARVQRVVGSAPAASLGIST-----GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 283:754-759(1998).
-- SIMILARITY: Belongs to peptidase family S2C.
-- SIMILARITY: Contains 2 PDZ/DHR domains.
-- SIMILARITY: Contains 2 PDZ/DHR domains.
-- THE AUTHOR: REF.1 SEQUENCE WAS INCORRECT: DUE TO SEQUENCING ERRORS THE AUTHORS TRANSLATED THEIR PUTATIVE 59 kDa IMMUNOGENIC PROTEIN ON THE COMPLEMENTARY STRAND TO THAT OF WHAT SEEMS TO BE THE REAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDDINE=90337348; PubMed=2279836;
Kahane S., Weinstein Y., Sarov I.;
"Cloning, characterization and sequence of a novel 59-kDa protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=D/UW-3/Cx;
PEDELINE=29008089;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                P18584; 084830;
01-NVV-1990 (Rel. 16, Created)
30-NRV-2000 (Rel. 39, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-) (59
immunogenic protein) (SK59).
                                                                                                                                                                                                                                                                                                                                                                               Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                       385 IITSVNGTKVSNGSDLYRILDQCKVGDEVTV 415
                                                                                                                                                     303 VITAVDGAPINSATAMADALNGHHPGDVISV 333
                                                                                                                                                                                                                                                         497 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHCI-2DPAGE; P18584; -.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001078; PDZ.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001256; Peptidase_S1B_V8.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
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PIR; H71465; H71465.
PHCI-2DPAGE; P18584; -.
                                                                                                                                                                                                                                                          STANDARD;
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Gene 90:61-67(1990).
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                                                                                                                                                                                                                                                                                                                  139 PSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQT----VQASDSLTGAEET 192
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PROBABLE SERINE PROTEASE DO-LIKE.
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SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease;
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June 30, 2004, 16:43:01; Search time 25.8569 Seconds (without alignments) 4331.879 Million cell updates/sec Run on:

US-09-597-796C-4 1802 1 MSNSRRRSLRWSWLLSVLAA.....QTKSGGTRTGNVTLAEGPPA 355 Title: Perfect score: Sequence:

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1017041 Total number of hits satisfying chosen parameters:

1017041 segs, 315518202 residues

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	007175 mycobacteri	Q7u2s9 mycobacteri	Q50320 mycobacteri	Q9ccy9 mycobacteri	Q8vka4 mycobacteri	Q7u0x2 mycobacteri	O53896 mycobacteri	Q9cd67 mycobacteri	Q9z5g6 mycobacteri	Q9fbk9 streptomyce	Q93j30 streptomyce	Q8dg87 synechococc	P72780 synechocyst	Q82fm9 streptomyce	Q82il8 streptomyce	Q8fr17 corynebacte
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ALIGNMENTS

	O07175 PRELIMINARY; PRT; 355 AA.			Hypothetical protein (Serine protease, putative). PEPA OR RV0125 OR MTC1418B.07 OR MT0133.	Mycobacterium tuberculosis.			•				Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,		Badcock K., Basham D., Brown D., Chillingworth T., Connor K.,	Davies R., Devlin K., Feltwell T., Gentles S., hamilin N., holitoyu		Oliver S., Osborne J., Quall M.A., Kajandream M.A., Kogers D.,			"Deciphering the blology	complete genome sequence.";			STRAIN=CDC 1551 / Oshkosh;	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L.,	Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,	Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg			"Whole genome comparison or Mycobaccerium cubercurosts crimical		
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MEDLINE=22709107; PubMed=12788972;
Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
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EMBL; Z66071; CAB09453.1; --
REMBL; Z66071; CAB09453.1; --
REMBL; AE006925; AAK44357.1; --
REMBL; AE006925; AAK44357.1; --
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable serine protease PEPA (EC 3.4.21.-).
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PROSITE; PS00135; TRYPSIN_SER; 1.
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SEQUENCE 35
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Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. US.A. 100:7877-7882(2003).
BMBL, BX248334, CAD922991.1; -
HYDROLASS. Complete proteome.
SEQUENCE 355 AA, 34926 WW; 16CE9E21A97BF192 CRC64;
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MEDLINE=95005449; PubMed=7921248;
MEDLINE=95005449; PubMed=7921248;
Cameron R.M., Stevenson K., Inglis N.F., Klausen J., Sharp J.M.;
Clantification and characterisation of a putative serine procease expressed in vivo by Mycobacterium avium subsp paratuberculosis.",
Microbiology 140:1977-1982(1994).
EMBL; Z23092; CAA80638.1;
PIR; S47170; S47170.
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                                                                                                                                                                                                                                  99.4%; Score 1792; DB 16; Length 355; 99.4%; Pred. No. 3.5e-87; tive 0; Mismatches 2; Indels 0.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0007429; F:trypsin activity; IEA.
GO; GO:0007429; P:intracellular signaling cascade; IEA.
GO; GO:000508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR0010303; Cys Ser_trypsin.
InterPro; IPR001189; PDZ.
InterPro; IPR001254; Peptidase_S1.
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Pfam, PF00089, trypsin, 1.
PRINTS, PR00834, PROTEASES2C.
SWART, SM00228, PDZ, 1.
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InterPro; IPR001478;
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X MEDLINE=2112872; Pubmed=11234002;

A GLINE=2112872; Pubmed=11234002;

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A Wheeler P.R., Bonore N., Garnier T., Churcher C., Harris D.,

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EMBL, AL583926; CAC32191.1; -.

BIR, AB7242, A87242.

BIR, A87242, A87242.

BIR, A87242, A87242.

BIR, AB7242, A87242.
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                                                                                                                                                                                                                                                                                                                                                                                                           61 AWGQYGPQVVNIDTKEGYNNAVGAGTGIVIDPNGVVLTNNHVISGATEISAFDVGNGQT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGVDVVGYDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGOGGTPRAVPGRV
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 15, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable secreted serine protease.
ML2659.
My20bacterium leprae.
Mycobacterium actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TAXID=1769;
                                                                                                                            Query Match 72.5%; Score 1306; DB 2; Length 3
Best Local Similarity 70.4%; Pred. No. 1.6e-61;
Matches 255; Conservative 41; Mismatches 58; Indels
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GO; GO:0007242; P.intracellular signaling cascade; IEA.
GO; GO:0006508; P.proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
                                          1 38 POTENTIAL.
361 AA; 35709 MW; 30FEF78FD6F3C411 CRC64;
      Hydrolase; Protease; Serine protease; Signal. SignAL 1 38 POTENTIAL.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
InterPro; IPRO03254; Peptidase S1.
InterPro; IPRO03256; Peptidase_S1B_V8.
InterPro; IPRO0326; Peptidase_S1C.
InterPro; IPRO0326; Poz; I.
InterPro; IPRO0334; PROTZASES.
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GO; GO:0007242; P:intracellular signaling cascade; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ.
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76 VGAGTGIVIDPNGVVLTNNHVIAGAT---
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                                                                                                                                                                                                                                       102 AASLVGFNRAPAGPSGGPVAASAAPSIPAANMPPGSVEQVAAKVVPSVVMLETDLGRQSE 161
                                                                                                                                                                                                                                                                                            AVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDS 185
                                                                                                                                                                                                                                                                                                                                                             240 AIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV-DNNGNGARVQRVVGSAPAASLGI 298
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                                                                                                                                                                                                                  75
                                                                                                                                                                                                             19 AAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSA---MVAQVAPQVVNINTKLGYNNA
                                                                                                                                                                                31; Gaps
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Best Local Similarity 36.0%; Pred. No. 2.9e-17;
Matches 127; Conservative 59; Mismatches 136; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
EMBL: BX248337; CAD93870.1; -
Hydrolase, Complete proteome.
SEQUENCE 464 AA; 46436 MW; AB93A4BB3FFA9BB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKGVVVTKVDDRPINSADALVAAVRSKAPGATVALTRQDPSGGSRTVQVTLGK 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRIGNVTLAE 351
                                                                                                                                             26.1%; Score 469.5; DB 16; Length 446; 36.0%; Pred. No. 2.8e-17; ive 59; Mismatches 136; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Probable serine protease (Serine proteinase) (EC 3.4.21.-).
                                                                                                              446 AA; 44484 MW; 54170CBEA8FE872B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 AA
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STRAIN-AF2122/97;
MEDLINE-22709107; PubMed=12788972;
InterPro; IPR001254; Peptidase S1
InterPro; IPR001940; Peptidase_S1
Pfam; PF00059; PDZ; 1.
PFam; PF00089; trypein; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
PROSTTE; PS50106; PDZ; 1.
SEQUENCE 446 AA; 44484 MW; 54
                                                                                                                                                                           Matches 127; Conservative
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Mycobacterium bovis.
                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     186
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19 AAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSA---MVAQVAPQVVNINTKLGYNNA 75

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408
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                                                                    238 AVVRVQGVSGLTPISLGSSSDLRVGQPVLAIGSPLGLEGT--VTTGIVSALNRPVSTTGE 295
                                                                                                                                239
                                                                                                                                                                                                     240 AIPIGGAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV-DNNGNGARVQRVVGSAPAASLGI 298
                                          AVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGOTVQASDS 185
                                                                                                                                                                      354
                                                                                                                                                       296. -AGNQNTVLDAIQTDAAINPGNSGGALVNMMAQLVGVNSAIATLGADSADAQSGSIGLGF
                                                                                                                                                                                                                                         355 AIPVDQAKRIADELISTGKA-----SHASLGVQVTNDKDTPGAKIVEVVAGGAAANAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98295987; PubMed=9634230;

Cole'S.T. Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Englmeier K., Parkhill J., Garnier T., Churcher C., Harris D., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Antersey T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Antersey T., Skelton S., Squares S., Squares R., Sulston J.E., Tablology G. Mycobacterium tuberculosis from the Tomphete genome Sequence...

Tomphete genome Sequence...

Tomphete genome Sequence...

Nature 393:537-544(1998).

--- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.

R PHR., C70821; C70821.

Tuberculist, RV0983; --
180 -- EGSGIILSAEGLILTNNHVIAAAKPPLGSPPPKTTVTFSDGRTAPFTVVGADPTSDI
                                                                                                                            86 LTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA----ASDNFQLSQG--GQGF
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                                                                                                                                                                                                                                                                                                299 STGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAE 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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GO:0004295; F:trypsin activity; IEA.
GO:0007242; P:intracellular signaling cascade; IEA.
GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001478; PDZ.
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Last annotation update)
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InterPro; IPR001940; Peptidase_SIC.
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASESZC.
SMART; SM00228; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative serine protease.
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Matches 127; Conserv
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                  120 AASLVGFNRAPAGPSGGPVAASAAPSIPAANMPPGSVEQVAAKVVPSVVMLETDLGRQSE 179
                                                    128 AVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDS 185
                                                                                                                                       296 -AGNONTVLDAIQTDAAINPGNSGGALVAMMAQLVGVNSAIATLGADSADAQSGSIGLGF 354
                                                                                                                                                                     240 AIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV-DNNGNGARVQRVVGSAPAASLGI 298
                                                                                                                                                                                                                                                                                                                                                                                                                         76 VGAGTGIVIDPNGVVLTNNHVIAGAT-----DINAFSVGSGQTYGVDVVGYDRTQDV 127
19 AAVGLGLATAPAQAAPPALSQDRFADFPALPLDPSA---MVAQVAPQVVNINTKLGYNNA 75
                                                                                                                            186 LIGAEETINGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA----ASDNFQLSQG--GQGF
                                                                                                                                                                                                                           409 PKGVVVTKVDDRPINSADALVAAVRSKAPGATVALTFQDPSGGSRTVQVTLGK 461
                                                                                                                                                                                                             299 STGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAE 351
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769;
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PIR, MESSOLI, MACADOSTI, T.

Leproma, MIGOTS, P.

Leproma, MIGOTS, P.

GO, GO:0008233; F:Pptidase activity; IEA.

GO; GO:0004225; F:trypsin activity; IEA.

GO; GO:0004225; F:trypsin activity; IEA.

GO; GO:000528; P:prtacellular signaling cascade; IEA.

GO; GO:000528; P:prtacellular signaling cascade; IEA.

InterPro; IPR001254; P:pptidase_SI.

InterPro; IPR001254; Peptidase_SI.

InterPro; IPR001254; Peptidase_SI.

Pfam; PP00089; PLYPSin; 1.

Pfam; PP00089; PROTEASESC.

SWART; SM00228; PDZ; 1.

RHYdrolase; Protease; Complete proteome.

SEQUENCE 382 AA; 37084 MW; 3DDBDDBAR32A80D CRC64;
                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                        PRT; 382 AA
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Possible secreted serine protease.
                                                                                                                                                                                                                                                                                        PRELIMINARY;
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269 GLGFAIPVDQAKRIADELISTG--KATH----ASLGVQVATDKGTPGAKVMDVVAGGAAA 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 TSDIAVVRVQSISGLTPITMGSSADLRVGQPVVAVGSPLGLAGT--VTSGIVSALNRPVS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 ASDSLIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAA-----SDNFQLSQG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 GOGFAIPIGOAMAIAGOIRSGGGSPTVHIGPTAFLGLGVVDNNGN-GARVORVVGSAPAA 294
                                                                                                                                                                                                                                                   78 AGTGIVIDPNGVVLTNNHVIAGA------TDINAFSVGSGQTYGVDVVGYDR 123
                                                                                                        22 GLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA----PQVVNINTKLGYNNAVG 77
                                                                                                                                                                         50 GAGPVIGPAASVPAAMM------PSGSVEQVAVKVVPSVVMLETDLGRQSE-- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 SLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRIGNVTLAE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 NAAVPKGVVLTKVDDRLISSADALVAAVRSKAPGDKVSLTYQDQSGSSRTVQVTLGK 379
Best Local Similarity 36.4%; Pred. No. 7.3e-17;
Matches 130; Conservative 52; Mismatches 121; Indels 54; Gaps
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MEDIJNE=93188700; PubMed=8446027;
Eiglimeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
"Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae.";
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769,
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RMEL; ALO35500; CAB36690.1; --
RMEL; ALO35500; CAB36690.1; --
RMEL; ALO35500; CAB36690.1; --
RMEL; ALO35500; CAB36690.1; --
RMEL; ALO35500; CAB36690.1; --
RGJ; GO:0008203; F:trypsin activity; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
R GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
R InterPro; IPR001204; Peptidase_S1.
R InterPro; IPR001204; Peptidase_S1.
R InterPro; IPR001304; Peptidase_S1.
R PEAN; PR00695; PTYPSin; 1.
R PEAN; PR00695; PTYPSin; 1.
R PEAN; PR00894; PROTEASES2C.
R SANAT; SM00220; PDZ; 1.
R Hydrolase; Protease; Serine protease.
SEQUENCE 452 AA; 45130 MW; 6CA675EB091IF983 CRC64;
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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222 TSDIAVVRVQSISGLTPITMGSSADLRVGQPVVAVGSPLGLAGT--VTSGIVSALNRPVS 279
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                                                                                                                                                                                                                                                                                                                          182 ASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAA-----SDNFQLSQG 235
                                                                                                                     GAGPVTGPAASVPAANM------PSGSVEQVAVKVVPSVVMLETDLGROSE-- 164
                                                                                                                                                                                                       165 EGSGVILSADGLILTNNHVVAVAAKPGGGPGGGLSPKTTVTFF---DGRTASFTVVGADP 221
                                                                                                                                                                                                                                           TQDVAVLQLRGAGGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQ 181
                                                                                                                                                                                                                                                                                                                                                                                                     GOGFAIPIGOAMAIAGOIRSGGGSPTVHIGPTAFLGLGVVDNNGN-GARVORVVGSAPAA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                          339 GLGFAIPVDQAKRIADELISTG--KATH----ASLGVQVATDKGTPGAKVMDVVAGGAAA 392
                                                                                 22 GLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVA----PQVVNINTKLGYNNAVG 77
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MEDLINE=S7000351; PubMed=8843436;
MEDLINE=S7000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of cordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
hol. Microbiol. 21:77-96(1996).
25.5%; Score 460; DB 2; Length 452;
36.4%; Pred. No. 9e-17;
ive 52; Mismatches 121; Indels 54; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative protease.
2055149 OR SCP8.12.
Streptomyces collicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Cerdeno A.M. - Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (4015-2000) to the EMBL/GenBark/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saunders D., Harris D.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
  Query Match
Best Local Similarity 36.4%
Matches 130; Conservative
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STRAIN=A3(2) / M145;
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                                                                                                                                                                                                                                               124
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Q9FBK9
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206 GVGTVELP-QAGPEAAERD------PDSVAGIAARALPSVVTLH--VSGSEAAGTGTG 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                              255 FVLDGRGHILTNNHVVEPAGSGGEITVTFNSGDTAEAEVVGRDSGYDLAVVKVKGVTGLT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 SAAIGG--GVAVGEPVVAMGNSGGGGTPRAVPGRVVALGQTVQA-SDSLTGAEETLNGL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 PMPLGNSDNVRVGDPVVAIGAPFDLAGT--VTSGIISAKERPITAGGEEGDGSDISYVDA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 IQFDAAIQPGDSGGPVVNGLGQVVGMNTA-----ASDNFQLSQGGQGFAIPIGQAM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 AIAGQIRSGGGSPTVHIGPTAFLGLGV-VDNN--GNGARVQ------RVVGSAPAASL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 RVAEEL-----INTGKAAHPVIGITLDMNYTGDGARVSAKGGDGGPAVTTGGPGAKA 484
                                                                                                                                                                                                                                                                                                                                                            22 GLGLATAPAQAAPPALSQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 GIKPGDVITAVDGQRVHSGEELIVKTRAHRPGDRLELTLQRDGKETKVSLVLGSSG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 GISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSGGTRTGNVTLAEG 352
                                                                                                                                                                                                                                                                                                                                46; Gaps
             "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                   22.6%; Score 407; DB 16; Length 542; 32.6%; Pred. No. 7e-14; ive 56; Mismatches 138; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                    STRAIN=A(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (UL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                           Hydrolase, Protease, Serine protease; Complete proteome.
SEQUENCE 542 AA; 53761 MW; 620F7D889DF7212D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                       116; Conservative
                           coelicolor_A3(2):";
Nature 417:141-147(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative protease.
SC03977 OR SCBAC25E3.14.
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Submitted (JUL-2001) to
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Hopwood D.A.;
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Matches
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us-09-597-796c-4.rspt

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VVGS-----APAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVNWQTKSG 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA----ASDNFQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSQCGQ---GFAIPIGQAMAIAGQIRSGCGSPTVHIGPTAFLGLGVVDNNGNGARV--QR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hopwood U.A.;

"Complete genome sequence of the model actinomycete Streptomyces celicolor A3(2):";

"Nature 417:41-447(2002)."

In Nature 417:41-447(2002).

BRBL; AL939118; CAC44701.1;

"RGO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0004295; F:prypsin activity; IEA.

GO; GO:0004295; F:prypsin activity; IEA.

GO; GO:0004295; F:prypsin activity; IEA.

InterPro; IPR001294; PpDZ.

InterPro; IPR001294; Peptidase S1.

InterPro; IPR001294; Peptidase S1.

InterPro; IPR001990; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

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InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

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InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptidase S1.

INTERPRO; IPR001991; Peptidase S1.

InterPro; IPR001991; Peptida
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STRAIN=A3(2) / MA4.
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; Nubmer R.D., Cardeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Fraser A., Gole, A., Hidalgo J., Hornsby T., Howarth S.,
Rubbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Hopwood D.A.;
                                                   STRAIN=A3(2);

REDINES-97000311; PubMed=8843436;

Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,

Kinashi H., Hopwood D.A.;

A set of ordered cosmids and a detailed genetic and physical map

the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.0%; Score 396; DB 16; Length 5: 32.2%; Pred. No. 2.5e-13; ive 54; Mismatches 148; Indels
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119; Conservative
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                      FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 BPVVAMGNSGGGGGTPRAVPGRVVALG--QTVQASDSLTGAEETLNGLIQFDAAIQPGDS 208
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SECURATE FOUNTAINS

MEDLINE=22225144; PubMed=12240834;

MEDLINE=22225144; PubMed=12240834;

MATANANINA Y., KANANINA K., KIMUTA T., KIShida Y.,

MATANANINA A., ITIGUCHI M., KAWASHIMA K., KIMUTA T., KISHIda Y.,

KIYOKAWA C., KOMATA M., MATSUMOCO M., MATSUMO A., NAKAZAKI N.,

KIYOKAWA C., SUGIMOCO M., TAKAUCHI M., TADATA S.;

MIMINOS W., SUGIMOCO M., TAKAUCHI M., TADATA S.;

MIMINOS W., SUGIMOCO M., TAKAUCHI M., TADATA S.;

MIMINOS RES., 9123-130(2002).

MATERIA APONGS37; BACO9988-1; -

GO; GO:000223; Fipeptidase activity; IEA.

GO; GO:000223; Fipeptidase activity; IEA.

GO; GO:000223; Fipeptidase activity; IEA.

GO; GO:000223; Fipeptidase activity; IEA.

GO; GO:000223; Fipeptidase S.;

INTERPO: IPRO01439; PD.:

MINTERPO: I
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                                                                                                                                                                                                                                                                                                                                Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
NCBL_TaxID=32046;
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                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                              update)
                                                                                                                                                            Created)
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                                                                                                                                                       (TrEMBLrel. 23,
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hes 108; Conservative
                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Serine protease.
                                                                                                                                                            01-MAR-2003
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Best Local S:
Matches 108
                                                                                  Q8DG87
RESULT 12
Q8DG87
                                                                                                                     SOW SERVICE STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STRE
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13 RESULT P72780

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334 SSSSGGLGSSGSIGLGFAIPINQAKYVAQELIKTGKPVYPVIGASVSLEEGTGGAKI 393
                                                                                                                                                 472 AA.
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InterPro; IPR001940; Peptidase_S1C.
                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 32.2%
                                                                                                                                                 PRELIMINARY;
                   312 INSATAM 318
                                                       350 ISDGARL 356
                                                                                                                                                                                                                                              Putative protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolites.";
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                                                                                                                                                 Q82FM9
                                                                                                                                                                   082FM9
                                                                                                            RESULT 14
Q82FM9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 LINAHVVDGASKV-VVTLRDGRIFDGQVRGTDEVTDLAVVKIEPQGSALPVAPLGTSSNL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 AVGEPVVAMGNSGGQGGTPRAVPGRVVALG--QTVQASDSLTGAEFTLNGLIQFDAAIQP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 GDSGGPVVNGLGQVVGMNTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 PTAFLGLGV---VDNNGN------GARVQRVVGSAPAASLGISTGDVITAVDGAP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 -VOMMNITVDQAQQNNRNPNSPFIIPEVDGILVMRVLPGTPAERAGIRRGDVIVAVDGTP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 WILSVIAAVGIGLATAP----AQAAPPA-----LSQDRFADFPALPLDPSAMVA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVAPOVVNINTK-------GAGTGIVIDPNGVV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 YLLAFAVGTAFGIANLPHAVAAADDLPPAPVITAQASVPLTSESFV-----AAAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAG-GLPSAAIG--GGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 QVGDWAIAVGNPVGLDNT-----VTLGIISTLGRSAAQAGIPDKRVEFIQTDAAINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84; Gaps
                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.2%; Score 382; DB 16; Length 394; 31.6%; Pred. No. 9.9e-13; ive 50; Mismatches 117; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase, Protease, Serine protease, Complete proteome.
SEQUENCE 394 AA, 41336 MW, AD59D94811B8F57B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.274; -.. GO; GO:0004295; F:trypsin activity; IEA. GO:0004295; F:trypsin activity; IEA. GO; GO:0007242; P:intracellular signaling cascade; IEA. GO; GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR009003; Cys_Ser_trypsin. InterPro; IPR001478; PDZ.
                                                                                                                          Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                      DNA RES. 3:109-136(1996).
-!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
EMBL; D90900; BAA16795.1; -
                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001254; Peptidase_S1.
InterPro; IPR008553; Peptidase_S1B_tx.
InterPro; IPR001256; Peptidase_S1B_V8.
InterPro; IPR001940; Peptidase_S1C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO1774; EXFOLTOXIN, PRINTS; PR00834; PROTEASES2C. PRINTS; PR00839; V8PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00228; PDZ; 1.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PSS0106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 31.6
Matches 116; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S74643; S74643
                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                 NCBI_TaxID=1148;
                                                                                                            HHOA OR SLL1679.
                                                                                        Protease HHOA
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53 SAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSV--GS 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GQTYGVDVVGYDRTQDVAVLQLRGA-GGLPSAAIGGG--VAVGEPVVAMGNSGGQGGTPR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 VITGIISAKNRPVASSDGSSSKASYMSALQTDASINPGNSGGPLLDAQGSVIGINSAIQ 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 ASDNFQLSQGGQ-----GFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFL-----GLGV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treda"H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microcranism Streptomyces avermilis.";
Nat. Biotechnol.;21:526-531(2003).
RMEL; AR0050318, BATT935.1;
GO; GO:0008233; F:rpptidase activity; IEA.
GO; GO:000823; F:rpptidase activity; IEA.
GO; GO:0007242; F:ntracellular signaling cascade; IEA.
GO; GO:000508; P:protecolysis and peptidolysis; IEA.
InterPro; IPR001478; PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 AVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Omura'S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hatrori M., "Genome sequence of an industrial microorganism Streptomyces avermitilis. deducing the ability of producing secondary
                                                                                                                                                                                                                   Bacteria; Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.2%; Score 382; DB 16; Length 4 32.2%; Pred. No. 1.2e-12; ive 57; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PP00595; PDZ; 1.
Pfam; PP00899; trypsin; 1.
PRINTS; PR00894; PROTEASESC.
SEQUENCE: COmplete protecome.
SEQUENCE: A72 AA; 46086 MW; AE04FAA409A3B7E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRLI 8165;
MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. [Natl. Acad: Sci. U.S.A. 98:12215-12220(2001).
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CENTRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

XX MEDLINE=22608306; PubMed=12692562;

XX MEDLINE=22608306; PubMed=12692562;

XB Interpro; Hatcorn M., Ourra S.;

Askair Y., Hatcorn M., Ourra S.;

Askair Y., Hatcorn M., Ourra S.;

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XY "Complete genome sequence and comparative analysis of the industrial

XY "Complete genome sequence and sequence and comparative analysis of the industrial

XY EMBL; AP005033; BAC708261;

XY GO; GO:0007422; Printracellular signaling cascade; IEA.

XY GO; GO:0007422; Printracellular signaling cascade; IEA.

XY GO; GO:0007422; Printracellular signaling cascade; IEA.

XY GO; GO:0007422; Printracellular signaling cascade; IEA.

XY GO; GO:000508; Printracellular signaling cascade; IEA.

XY InterPro; IPR001254; Peptidase—SI.

XY InterPro; IPR001940; Peptidase—SIC.

XY FEAM; PRO0895; PRDZ; 1.

XY SYMART; SM00284; PROTEASES2C.

XY SYMART; SM00284; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 SEERAADSVA-----GIAARALPSVVTLHVK--GSAAEGTGFVLDGRGHILFINNHVV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 -- AGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGG--GVAVGEPV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 VAMGNSGGOGGTPRAVPGRVVALGOTVQA-SDSLTGAEETLNGLIQFDAAIQPGDSGGPV 212
275 VDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVN 334
                        38 SQDRFADFPALPLDPSAMVAQVAPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVI 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
21.2%; Score 382; DB 16; Length 619;
Best Local Similarity 33.7%; Pred. No. 1.7e-12;
Matches 114; Conservative 53; Mismatches 127; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN=MA-4680 / Arcc 31267 / NCIMB 12804 / NRRL 8165;

MEDLINE=21477403; PubMed=11572948;

MEDLINE=21477403; PubMed=11572948;

Omura S., Ikeda H., Ishikawa U., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M.;

"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 619 AA; 64251 MW; D2D3C72A67D3B3A6 CRC64;
                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                     619 AA.
                                                                                                                                                                                                                                       PRT;
                                                                                                                  : |: | : | | | | 452 Y-TRDGKARTTDVTLGE 467
                                                                                     335 WOTKSGGTRTGNVTLAE 351
                                                                                                                                                                                                                                   Q821L8
Q821L8;
Q821L8;
O1-JUN-2003 (TrEMBLrel. 24, C)
O1-JUN-2003 (TrEMBLrel. 24, Lk)
O1-OCT-2003 (TrEMBLrel. 25, Lk)
Putative serine proteinase.
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Scoring table:

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

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SUMMARIES

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ALIGNMENTS

RESULT 1

Antigen, immunogen, vaccine, tuberculosis, non specific adjuvant, skin testing; M.tuberculosis. Mycobacterium tuberculosis antigen TbH-9FL. AAW32381 standard; protein; 391 AA. 95US-00523435. 95US-00532136. 96US-00620280. 96US-00658800. 96US-00680573. 96WO-US014675. Mycobacterium tuberculosis. (first entry) WO9709429-A2 30-AUG-1996; 13-JAN-1998 12-JUL-1996; 13-MAR-1997. 01-SEP-1995; 22-SEP-1995; 22-MAR-1996 05-JUN-1996 AAW32381; AAW32381

Campos-Neto A, Dillon DC, Twardzik DR; Skeiky YAW, (CORI-) CORIXA CORP. Reed SG, Sk Vedvick TH,

Houghton R;

WPI; 1997-192904/17. N-PSDB; AAT91455 New immunogenic polypeptide (s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection.

Example 3; Page 150-152; 190pp; English.

A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M. tuberculosis antigen, TbH-9FL The immunogenic polypeptide can be used to diagnose the tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen,

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Tuberculosis;
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especially monoclonal antibodies or equivalent polyclonal antibodies, also used for diagnosis
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                                                                                                                                   A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TbH-9FL The immunogenic protein, and fusion proteins containing one or more of the proteins proteins preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121. LIATNILGONTPAIAVNEAEYGEMWAQDAAMFGYAATATATATLEPEEAPEMTSAGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection; diagnosis; antigen; TbH-9FL.
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1949; DB 2;
100.0%; Pred. No. 1.2e-142;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis; strain H37Rv
                                                                                               English
                                                                                            Example 3; Page 138-139; 168pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW64335 standard, protein, 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches "391; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           Sequence 391 AA;
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TB;

protective immunity;

Houghton R;

Campos-Neto A,

Dillon DC, C DR, Lodes MJ;

96US-00730510. 97US-00818112. 97WO-US018293.

CORP

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This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used develop products for the detection of M. tuberculosis infection and fidagnosis; treatment and prevention of tuberculosis.
tuberculosis immunogenic polypeptide TbH-9FL
                                                 Tuberculosis, immunogenic, soluble, antigen, p
vaccine, pharmaceutical, infection, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3B; Page 128-129; 230pp; English.
                                                                                                                           Mycobacterium tuberculosis.
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N-PSDB; AAV64503.
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                                                                                                                                                                                                                                                                              07-OCT-1997;
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13-MAR-1997;
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Vedvick TS,
                                                                                                                                                                                                                            23-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide comprises Mycobacterium tuberculosis antigen TbH-9FL. It is encoded by genomic DNA (see AAV44395) isolated from a M. tuberculosis strain H37Rv genomic DNA (see AAV44395) isolated from a M. tuberculosis AAV44371). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a Soluble M. tuberculosis antigen, or an immunogenic portion of a Soluble M. tuberculosis antigen, or an immunogenic portion of a Soluble M. tuberculosis antigen, as well as DNA transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient will primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to transfarence OS field)
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                                                                                                                                                                                                                                                   New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
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                                                                                                      Houghton R;
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                                                                                                 Skeiky YAW, Dillon DC, Campos-Neto A, S, Twardzik DR, Lodes MJ;
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     97US-00818111
                                                    (CORI-) CORIXA CORP.
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                                                                                                                                                                                                    N-PSDB; AAV44395
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     13-MAR-1997;
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                                                                                                   Reed SG,
Vedvick
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Query Match 100.0%; Score 1949; DB 2; Length 391; Best Local Similarity 100.0%; Pred. No. 1.2e-142; Matches 391; Conservative 0; Mismatches 0; Indels 0.
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RESULT

(first entry

27-JAN-1999

AAW81702,

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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                                                                                                          Mycobacterium tuberculosis
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N-PSDB; AAZ19093.
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Vedvick TS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
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                                                                                                        Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection.
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Pred. No. 1.2e-142;
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              standard; protein; 391
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97FR-00011325
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Goguet De La Salmoniere
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                                                                                                                                                                                                                                                                                                                                                                                        protein expression
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                                                                                                                                          Mycobacterium
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Best Local
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LIEGAAAVEEASDTAAANOLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
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RC;
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100.0%; Pred. No. 1.2e-142;
iive 0; Mismatches 0;
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361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                               AAY38989 standard, protein; 391
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vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Age can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to AAX39225 are used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are avecines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. W. tuberculosis Ag's. DiMs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               skin
                                                                LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPPARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antigens from Mycobacterium tuberculosis useful in diagnostic tests and protective or therapeutic vaccines or compositions.
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                                                                                                                                                                                                                                                                                                                               s; M. tuberculosis; antigen; immun
immunisation; vaccine; infection;
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), Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                  M. tuberculosis antigen TbH-9FL amino acid sequence.
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100.0%; Pred. No. 1.2e-142;
ive 0; Mismatches 0;
                                                                                                      GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                           GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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                                                                                                                                                                                                           AAY39132 standard; protein; 391 AA.
                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis; M.
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                                                                                                                                                                                                                                                                                                                                                             immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                diagnosis;
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05-MAY-1998;
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The sequence represents Mycobacterium tuberculosis TbH9 (also known as Mtb3A), an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
                                                                                                                                                                         240
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                                                                                                                                                                                                                           LIEGAAAVEBASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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                                                                                                       LIATNILIĞÜNTPAIAVNEAEYGEMWAQDAAMFGYAAATATATATLIPFEFAPEMTSAGG
                                                                                                                                                                            LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                             MVSMANNHMSMINSGVSMINILSSMLKGFAPAAAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                           LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TbH9; Mtb39A; antigen; vaccine; tuberculosis; AIDS; acquired immunodeficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcneill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. tuberculosis antigen TbH9 (Mtb39A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU01888 standard; protein; 391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghton RL,
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99US-0158425P.
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61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120

1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60 WUDFGALDPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60

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(CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                              New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium
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                                                                           MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                          SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                      SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                Gaps
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                Indels
 Pred. No. 1.2e-142;
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                 Mismatches
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                 Conservative
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 Best Local Similarity
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N-PSDB; AAD47082.
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                 Matches 391;
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from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention user used in methods for eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mycobacterium sp. TDH9FL antigenic protein
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                                                                                                                                                                                                                                                      391;
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100.0%; Pred. No. 1.2e-142;
tive 0; Mismatches 0;
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01-FEB-2001; 2001US-0265737P.
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for elliciting an immune response in a mammal, e.g., human, immunised with BCC. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymorlectices are useful in the diagnosis, treatment and prevention of Mycobacterium in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis to generate or monitoring of disease progression, as immunogens to generate or ellicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human called in proteins of the invention are also used as vaccines. MTB32A fusion proteins of the invention are also used as vaccines. MTB32A fusion proteins of the invention are also used as vaccines. MTB32A fusion proteins of the invention are also used as vaccines.
                                                        Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                Claim 83; Page 102-103; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTB39 (TbH9) protein
N-PSDB; AAD28341
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Sequence 391 AA;

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LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGFGQMLGGLFV 360
                                                                                                                                                                                                                                                                                                                                                                                                        LIAINLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 180
                                                                                                                                                                                                                                                      LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                                                                                                                                    MYSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                                                                                           SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
                                                                                                                                                      SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
                                                                                                                                                                                                                       LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGG 180
                                                               60
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                                                                                   MYDFGALPPEINSARMYAGPGSASLVAAAQMHDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                               WVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-142;
Matches 391; Conservative 0; Mismatches 0; Indels 0
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AAY32070 standard; protein; 596
RESULT 11
       AAY32070
ID AAY3
XX
AC AAY3
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DT 17-J
XX
DB Mycco
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Mycobacterium tuberculosis antigen fusion protein Mtb59f.
(first entry)
  17-JAN-2000
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AAY32070;

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241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a recombinant Mycobacterium tuberculosis biantigan fusion protein, termed Mtb59f, composed of the antigens TbH9 and Rais. The fusion protein is expressed in host cells using a vector carrying a polymucleotide (see AAZ20205) comprising the coding sequences for the 2 antigens. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WVDFGALPPEINSARMYAGPGSASIVAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIAINLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis.
        Tuberculosis, antigen, fusion protein, Mtbs9f, TbH9, Ra35, diagnosis, therapy, vaccine, immunogen.
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/note= "Met/His tag"

                                                                                          Location/Qualifiers
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                                                                                                                                                    /note= "Ral2"
143. .596
/note= "TbH9"
                                                                                                                                                                                                                                                                                  99WO-US007717.
                                                                                                                                                                                                                                                                                                                98US-00056556.
98US-00223040.
                                                          Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                             Skeiky YAW, Alderson M,
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Matches 391; Conservative
                                                                                                                                         9. .140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                  07-APR-1999;
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30-DEC-1998;
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9 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG

SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 69 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAAYETAYGLTVPPPVIAENRAELMI

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LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                                                                                                                                                                                                                                                                                                                              recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, or 6H polynucleotide, useful as vaccine to elicit protective immunity .nst pathogenic microorganisms e.g. Leishmania and Mycobacterium
                                                                                                                                                                              Vaccine, immunity, diagnostic agent, gene therapy, TbH9, antigen, Ra35, MTB59F; fusion protein.
                                    GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                   GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                            Mycobacterium sp. MTB59F fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 98-99, 155pp, English.
                                                                                                                                                                                                                                                                                                                                   Guderian J;
                                                                                               AAE29710 standard; protein; 596
                                                                                                                                                                                                                                                                               13-MAR-2002; 2002WO-US008223.
                                                                                                                                                                                                                                                                                               13-MAR-2001; 2001US-0275837P.
                                                                                                                                                                                                       Mycobacterium sp.
Mycobacterium tuberculosis.
                                                                                                                                          (first entry)
                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                   Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                   2002-759844/82.
                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD47086
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tuberculosis.
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27-JAN-2003
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301
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                                                                                                                 AAE29710;
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309 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 368

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369 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391

361

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AAE17574 standard; protein; 596 AA

53

RESULT AAE1757

AAE17574;

249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 308 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360

241. MVSMANNHIMSMTNSGVSMTNTLSSMLKGPAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG

LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 189 LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN

LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 129 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG

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Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human,
                                                                                                                     Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB59F; TbH9-Ra35 protein.
                                                                                    Mycobacterium species MTB59F fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 114-115; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky Y, Reed S, Alderson M;
                                                                                                                                                                                                                                                                              20-JUN-2001; 2001WO-US019959.
                                                                                                                                                                                                                                                                                                           20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-147798/19.
                                                                                                                                                                         Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-147798
N-PSDB; AAD28344
                                                                                                                                                                                                          WO200198460-A2.
                                                   22-APR-2002
                                                                                                                                                                                                                                             27-DEC-2001
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA. LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic

microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human

animal. The invention is used in gene therapy. The present sequence is MTB3SP fusion protein. This fusion protein comprises Ra35 protein from Mycobacterium tuberculosis and TbH9 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)

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0; Gaps

Length 596; Indels

Score 1949; DB 5;
Pred. No. 2.1e-142;
0; Mismatches 0;

100.0%;

Query Match Best Local Similarity 100.(Matches 391, Conservative

Sequence 596 AA;

us-0y-5y/-/yoc-8.rag

immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species MTB59F (TbH9-Ra3S) fusion protein

Sequence 596 AA;

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                                                                                                                                                                                              MVSMANNHMSMINSGVSMINILSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
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                                                     MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                            LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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100.0%; Score 1949; DB 5; Length 596; 100.0%; Pred. No. 2.1e-142; ive 0; Mismatches 0; Indels 0;
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                     Matches 391; Conservative
           Local Similarity
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Fusion protein; tuberculosis; Mycobacterium tuberculosis; tuberculostatic; immunogen; vaccine; Tb59-Ra35; Mtb59f.
                                                                  Antigenic fusion protein Tb59-Ra35 (Mtb59f)
                                                                                                                             Location/Qualifiers
             standard; protein;
                                                                                                        Mycobacterium tuberculosis.
                                            (revised)
(first entry)
                                            29-AUG-2003
08-MAY-2002
                             AAU74599;
               AAU74599
                                                                                                               Chimeric
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300

128 180 188 240 248

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/label= OTHER /note= "OTHER= Xaa. Xaa= In frame stop codon" Key Misc-difference

US2002009459-A1

24-JAN-2002

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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYSMANNHMSWTINSGVSWIINTILSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                          New fusion proteins of Mycobacterium tuberculosis antigens, useful diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1949; DB 5; Length 599; 100.0%; Pred. No. 2.1e-142; Live 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                         Alderson
                                                                                                                                                                                                       Dillon DC,
                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 12; 62pp; English
                                     97US-00818112.
97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
           99US-00287849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 391; Conservative
                                                                                                                      REED S G.
SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A.
                                                                                                                                                                                                       Reed SG, Skeiky YA,
                                                                                                                                                                                                                                    WPI; 2002-171134/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 599 AA;
                                                                                                                                                                                                                                                  N-PSDB; ABK14139
                             13-MAR-1997;
01-OCT-1997;
18-FEB-1998;
07-APR-1998;
30-DEC-1998;
             07-APR-1999;
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15 RESULT

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301 IGGGVAANIGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                              309 IGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 368
                                                                                                                         369 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                               361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                              Search completed: June Job time : 41.2057 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen fusion protein, termed Mtb61f, composed of the antigens TbH9, DPV and MTI. The fusion protein is expressed in host cells using a vector carrying a polymucleotide (see AAZ20203) comprising the coding sequences for the 3 antigens. The invention provides fusion proteins (see AAX2059-11) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polymucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                      Tuberculosis, antigen, fusion protein, Mtb61f, TbH9, DPV, MTI, diagnosis, therapy, vaccine, immunogen.
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Best Local Similarity 100.0%; Pred. No. 2.1e-142;
Matches 391; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campos-Neto A;
                      AAY32068 standard; protein; 600 AA
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98US-00223040.
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N-PSDB; AAZ20203.
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30-DEC-1998;
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OM protein - protein search, using sw model

June 30, 2004, 16:44:57; Search time 11.8942 Seconds (without alignments) 1697.113 Million cell updates/sec Run on:

US-09-597-796C-8 1949 1 MVDFGALPPBINSARMYAGP.....SGVLRVPPRPYVMPHSPAAG 391 Title: Perfect score:

Sequence:

389414 seqs, 51625971 residues Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

389414

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	-107 Sequence 107	-102 Sequence 102	-107 Sequence 107	-102 S	-107 Sequence 107	6 Sequence 26,	-22 Sequence 22,	-2 Sequence 2,	-2 Sequence 2,	equence 111	-106 Sequence 106	-111 Sequence 11:	-106 Sequence 106	-111 Sequence 11:	-109 Sequence 109	10	-109 Sequence 109	-104 Sequence 10	09 Sequence 103	9-8 Seguence 8,	1 Sequence 91	-92 Sequence 92	-91 Sequence 91	6-92 Sequence 92	7-91 Sequence 91	9-126 Sequence 12	0.00
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	5 2 4	Score 1949; Pred. No. 2
Application US/08818112 00969 WAMION: Reed, Steven G. Skeiky, Yasir A.W. Dillon, Davin C. Campos-Neto, Antonio Houghton, Raymond Vedvick, Thomas S. Twardzik, Daniel R. TWardzik, Daniel R.	Y L L nte	(
i t i ge A ke	DENCES: SEED and BERRY IOO COLUMBIA Centerties with the state of the s	
T 1 1 UBB 112-107 UBB 112-107 UBB 107, Application ENT No. 6290969 NERAL INFORMATION: APPLICANT: Reed, Stev APPLICANT: Skeiky, Ya APPLICANT: Campos-Not APPLICANT: Vedvick, TAPPLICANT: TAPPL	NOWBER OF SEQUENCES: ADDRESSER: SEED and BERRY IN STREET: 6300 Columbia Center CITY: Scattle Nashington CITY: Scattle Nashington COUNTRY: Washington USA ZIP: Washington NASTER COUNTRY: WASHINGTON COUNTRY: WASHINGTON COUNTRY: WASHINGTON COUNTRY: WASHINGTON COUNTRY: WASHINGTON NASE: Bateful Release CONFURER: BATEFUL NATUR OF PATING SYSTEM: PC-DOS/MS CONFURER: WASHINGTON: APPLICATION NUMBER: US/08/8 FILING DATE: 13-MAR-1997 CLASSIFICATION NUMBER: US/08/8 ATTORNEY/AGENT INFORMATION: NAME: MAKI, DAYIG J. TELECHONIC: (206) 682-6031	Match Local Similarity
107, A) 107, A) 6290 INFORM ANT: ANT: ANT: ANT: ANT: ANT: ANT: ANT:	MAGEN OF SEQUENT PRESCRIPTION OF SEATURE STATE: 6300 CITY. SCATE: MASHIN COUNTRY: USA COMPUTER: BADABIN TO SET OF SEATURE STATE: BASEN OF SEATURE SEADABIN TYPE: COMPUTER: BASEN OF SEATURE SE	cch al Simi
RESULT 1 105-08-818-112-107 Sequence 107, Applica PATENTIAL INFORMATION: GENERAL INFORMATION: APPLICANT: Skeiky APPLICANT: Skeiky APPLICANT: Hought APPLICANT: Hought APPLICANT: Tampon APPLICANT: Tampon APPLICANT: Hought APPLICANT: Tampon APPLICANT: Tampon APPLICANT: Tampon APPLICANT: Tampon APPLICANT: Tampon APPLICANT: Tampon TITLE OF INVENTION: TITLE OF INVENTION:	NOWBEK OF SEQUENCY ADDRESSER: SEE STREET: 6300 CG CTTY: Seattle CTTY: Seattle CTTY: Seattle CTTY: Washingt COUNTY: WASHINGT CONFUTER READALE MEDIUM TYPE: F COMPUTER READALE COMPUTER READALE SOFTWARE: FEE COMPUTER: IBM OPERATING SYSTE SOFTWARE: FEE COMPUTER: IDM OFFERTING SYSTE SOFTWARE: FEE COMPUTER: IDM OFFERTING SYSTE SOFTWARE: FEE COMPUTER: IDM OFFERTING SYSTE SOFTWARE: FEE COMPUTER: IDM OFFERTING SYSTE TELEPHON INDM REFERENCE/DOCKE TELEPHONE: (206) INPORMATION IND REFERENCE/DOCKE TELEPHONE: (206) INPORMATION TOR SEQ SEQUENCE CHARACTE LENGTH: 391 am TYPE: amino ac STRANDEDNESS: TOPOLOGY: Inne COPOLOGY: Inne	Query Match Best Local
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COPPUINDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY ilp
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle.
STREET: Washington
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                                Length 391;
                                                                          Indels
                        Query Match 100.0%; Score 1949; DB 4; Best Local Similarity 100.0%; Pred. No. 2.9e-154; Matches 391; Conservative 0; Mismatches 0;
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
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Patent No. 6350456
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MACL, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPAN: (206) 682-6931
INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
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APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SEED and BERRY 1LP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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NAME: Maki, David J.
EGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INPORMATION FOR SEQ ID NO: 102: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SURFERT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 102, Application US/08818111
; Patent No. 6388852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-818-111-102
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US-08-818-111-102
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                                                                                                                                                                            100.0%; Score 1949; DB 4;
100.0%; Pred. No. 2.9e-154;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Slilon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Houghton, Raymond APPLICANT: Houghton, Raymond APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METITLE OF INVENTION: AND DIAGNOSIS OF NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 107; Application US/09072967; Patent No. 6592877; GENERAL INFORMATION:
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 391; Conservative
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MEDIUM TYPE: Floppy
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STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: USA
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US-09-072-967-107
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                                              100.0%; Score 1949; DB 4; Length 391; 100.0%; Pred. No. 2.9e-154; ive 0; Mismatches 0; Indels 0.
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APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardaik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
CORRESPONDENCE: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Columbia Center, 701 Fifth Avenue
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 102, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEED and BERRY LLP
                                                     Query Match
Best Local Similarity 100.
Matches 391; Conservative
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
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US-09-072-596-102
             US-09-056-556-107
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APPLICANT: Reed, Steven G.
APPLICANT: Seiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Dilangeria Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: 1999-04-07
TITLE OF TILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR APPLICATION NUMBER: US 09/025,040
PRIOR APPLICATION NUMBER: US 09/025,040
PRIOR APPLICATION NUMBER: US 09/025,040
PRIOR APPLICATION NUMBER: US 09/025,040
PRIOR APPLICATION NUMBER: US 09/025,040
PRIOR APPLICATION NUMBER: US 09/025,040
PRIOR APPLICATION NUMBER: US 09/025,040
PRIOR FILING DATE: 1998-12-30
NUMBER: OF SEQ ID NOS: 46
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                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
US-09-287-849-26
                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Best Local Similarity 100.0%; Pred. No. 5.2e-154;
Matches 391; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SSOFTWARE: PARENTIN Ver. 2.1
SSQ ID NO 26
LENGTH: 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/09287849
Patent No. 6627198
                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Reed, S
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
FILE REPRENCE: 014058-000402003
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
FRIOR APPLICATION NUMBER: US 08/925,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/056,556
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100.0%; Score 1949; DB 4; Length 391;
Best Local Similarity 100.0%; Pred. No. 2.9e-154;
Matches 391; Conservative 0; Mismatches 0; Indels 0
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Patent No. 6627198
GENERAL INFORMATION:
               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6910
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Best Local 8
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502 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
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US-09-287-849-2
; Sequence 2, Application US/09287849
; Patent No. 6627198
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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; Sequence 2, Application US/09223040
; Patent No. 6544522
; GENERAL INFORMATION:
; APPLICANT: Skelky, Xasir
; APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: Fusion Tritle OF INVENTION: Fusion Theory
; TITLE OF INVENTION: Fusion Theory
; TITLE OF INVENTION: and Their Uses
; FILE REFERENCE: 014058-009010US
; CURRENT APPLICATION NUMBER: US/09/223,040
; CURRENT FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                      69 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 128
                                                                                                                                                                                                                                                                                                                                                            LIATNILIGGNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEEAPEMTSAGG 180
                                                                                                                                                                                                                                                                                                                                                                              181 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
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; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-223-040-2
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                                                                                 FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-22
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                                                                                                                                                  Query Match 100.0%; Score 1949; DB 4; Length 600; Best Local Similarity 100.0%; Pred. No. 5.2e-154; Matches 391; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 729;
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llarity 99.7%; Pred. No. 1.8e-153;
Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
 PatentIn Ver. 2.1
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Best Local Similarity
Matches 390; Conservat
SOFTWARE: Pat
SEQ ID NO 22
LENGTH: 600
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LENGTH: 729
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US-09-223-040-2
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Blook, Mark
APPLICANT: Dillor, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANTON: and Their Uses
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 1996-00200S
CURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR PLILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR PLILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR PLILING DATE: 1998-04-07
PRIOR PLILING DATE: 1998-04-07
PRIOR PLILING DATE: 1998-12-30
SUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
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                                                                          LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGG 180
                                                                                                                                                                                                                    MVSMANNHMSMINSGVSMINILSSMLKGFAPAAAAQAVQIAAQNGVRAMSSLGSSLGSSG 300
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202 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAXETAYGLTVPPPVIAENRAELMI
                                                                                                           1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                      LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
VS-09-287-849-2
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99.7%; Score 1944; DB 4; Length 729;
Best Local Similarity 99.7%; Pred. No. 1.8e-153;
Matches 390; Conservative 0; Mismatches 1; Indels
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US-08-818-111-106
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US-08-818-111-106
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LIATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG 180
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                                                                    LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                    322 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                        MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Read, Steven G.
APPLICANT: Reid, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twandzik, Daniel R.
APPLICANT: Wolvick, Daniel R.
TITLE OP INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OP INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION WHERE: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
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84.9%; Pred. No. 1.4e-
live 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 111, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 84.9%
Matches 337; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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US-08-818-112-111
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                              MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL 296
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1 VVDFGALPPEINSARMYAGPGSASLVAAARKMDSVASDLFSAASAFQSVVWGLTTGSWIG 60
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61 SSAGLMVAAASPYVAMMSVTAGGAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardaik, Daniel R.
APPLICANT: Twardaik, Daniel R.
APPLICANT: TWARNING COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 GLPVGOMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 391
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT.APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210121.417C6
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Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION UNDER: 21012
REFERENCE/DOCKET NUMBER: 21012
REFERENCE/COCKET NUMBER: 21012
REFERENCE/COCKET NUMBER: 21012
REFERENCE/COCKET NUMBER: 21012
RELEFAX: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 106: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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N: 424
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TYPE: amino acid
STRANDEDNESS:
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APPLICANT: Reed, St
APPLICANT: Skeiky,
APPLICANT: Dillon,
APPLICANT: Campos-h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 CO
CITY: Seattle
STATE: Washingt
COUNTRY: USA
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                                                                                                                                        61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVATAENRAELMI
                                                                                                               1 MVDFGALPPEINSARWYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                7;
                 Query Match 84.8%; Score 1652.5; DB 4; Length 396; Best Local Similarity 84.9%; Pred. No. 1.4e-129; Matches 337; Conservative 19; Mismatches 34; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardaik, Daniel R.
APPLICANT: Twardaik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Codes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: WITHER OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTONREY/AGENT INFORMATION:
NAME: MAXI, DAVIG J.
REGISTRATION NUMBER: 31,392
RESTERNOR/DOCKET NUMBER: 210121.417C9
TELECOMMULCATION INFORMATION:
TELECOMMULCATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 106, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSE: SEED and B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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US-09-072-596-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 356
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US-09-056-556-111

Sequence 111, Application US/09056556

Patent No. 6350456

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth ***
CITY: Seattle
STREET: Washington
COUNTRY: USA
                                                                                                                                   1 VVDFGALPPEINSARMYAGFGSASLVAAAKMMDSVASDLFSAASAFQSVVWGLTTGSWIG
                                                                                                                                                                                                                          61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                 Gaps
                                                 ..
    DB 4; Length 396;
  84.8%; Score 1652.5; DB 4; Length
84.9%; Pred. No. 1.4e-129;
live 19; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
NAME: Maki, David J.
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 396 amino acids
amino acid
Query Match
Best Local Similarity 84.9
Matches 337; Conservative
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US-09-056-556-111
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357 GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 391
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OF TUBERCULOSIS
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                                                                              210121.411C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reed, Steven G.
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE: OF INVENTION: AND DIAGNOSIS OF
NUMBER OF SEGUENCES: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 109, Application US/08818112 Patent No. 6290969
  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REPRENCE/DOCKET NUMBER: 2101;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206):622-4900
TELEPHONE: (206):622-4900
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                            LENGTH: 396 amino acids
TYPE; amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.98
Matches 3377, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-09-072-967-111
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US-08-818-112-109
                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVSMANNHWSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVFAMSS----LGSSL 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 356
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                                                                                                                                                                                              Gaps
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Sequence 111, Application US/09072967

Sequence 111, Application US/09072967

SEQUENCE INFORMATION:

APPLICANT: Read, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Houghton, Raymond

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Lodes, Michael J.

APPLICANT: Codes, Michael J.

APPLICANT: Codes, Michael J.

APPLICANT: Hendrickson, Ronald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

CORRESPONDENCE ADDRESS:

ADDRESSED and PERFORMATION: SEED and PERFORMATION:

STREET: SEED and PERFORMATION:

STREET:
                                                                                                                                                                                            7;
                                                                                                                                                    84.8%; Score 1652.5; DB 4; Length 396;
84.9%; Pred. No. 1.4e-129;
ive 19; Mismatches 34; Indels 7;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
                                                                                                                                                                    Best Local Similarity 84.9
Matches 337; Conservative
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STATE: Washing
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                                                                          STRANDEDNESS
                                                                                                                US-09-072-596-106
                                                                                                TOPOLOGY:
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121 LIATNILGONTPALAVNEAEYGEMWAQDAAMFGXAATAATEALLPFEDAPLITNFGG 180
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                                                                                                                         1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                     Gaps
                                                                 7 ;
84.8%; Score 1652.5; DB 4; Length 396;
84.9%; Pred. No. 1.4e-129;
tive 19; Mismatches 34; Indels 7;
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240

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181 LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 VSSIANNHMSKMGTGVSMTNTLHSMLKGLAP-AAAQAVETAAENGVWAMSSLGSQLGSSL 299
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Pest Local Similarity 84.2%; Pred. No. 7.9e-116;
Matches 303; Conservative 16; Mismatches 36; Indels 5;
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PULING DATE: 13 MAR.1997
FILING DATE: 13 MAR.1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: MAK!, David J. 392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECHMANICATION INFORMATION:
TELEPRACE (2006) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-818-112-109
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Search completed: June 30, 2004, 16:55:19 Job time: 12.8942 secs



Sequence 12, Appl Sequence 4, Appli Sequence 18, Appl Sequence 17, Appl Sequence 16, Appl

Sequence Sequence Sequence 16, Sequence 2, A

Sequence 2, Appliance 2, Appliance 16, Appliance 16, Appliance 16, Appliance 16, Appliance 16, Appliance 16, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 110, Appliance 110, Appliance 110, Appliance 110, Appliance 110, Appliance 110, Appliance 110, Appliance 110, Appliance 110, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 111, Appliance 112, Ap

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61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09886349A;
Sequence 14, Application US/09886349A;
Publication No. US20040086523A1
GENERAL INFORMATION:
APPLICANT: Read, Steven
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: APPLICANTON WUMBER: US/09/886,349A
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2001-02-01
NUMBER: OF SEQ ID NOS: 50
SEQ ID NO 14
LENGTH: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 100.0%; Score 1949; DB 12; Length 391; al Similarity 100.0%; Pred. No. 1e-145; 391; Conservative 0; Mismatches 0; Indels 0;
US-10-282-122A-62027
                                                                                                                                                                                                                                                                                  US-10-098-732A-12
US-09-073-009-126
US-09-793-306-126
                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: MTB39 (TDH9FL)
US-09-886-349A-14
   RESULT 1
US-09-886-349A-14
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Best Local S:
Matches 391,
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Sequence 102, App
Sequence 14, Appl
Sequence 26, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence 21, Appl
                                                                             June 30, 2004, 16:52:58; Search time 30.4893 Seconds (without alignments) 3625.462 Million cell updates/sec
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                                                                                                                        US-09-597-796C-8
1949
1 WVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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| cgn2 6/ptodate/2/pubpaa/PCT_NEW_PUBCOMB.pep:*
| cgn2 6/ptodate/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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| cgn2 6/ptodata/2/pubpaa/USO9B_PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO0B_PUBCOMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-886-349A-14
US-10-193-002-102
US-10-098-732A-14
US-09-287-849-26
US-09-287-849-20
US-09-287-849-22
US-10-359-460-22
US-10-369-988-349A-18
US-10-369-988-349A-18
US-10-369-988-328-18
US-10-369-988-388-18
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                                                                                                                                                                                                   1166195 seqs, 282705291 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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                                                          protein
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.61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
                                                                                                                                                                                                                                                                                                                  121 LIATNLLGQNTPAIAVNBAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 180
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                                                                                               1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                             1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                         61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                   121 LIATNILGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATLILPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skelky, Yasir A.W.

Skelky, Yasir A.W.

Dillon, Davin C.

Campos Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.

Twardzik, Thomas S.

Twardzik, Daniel R.

Lodes, Michael J.

Hendrickson, Romald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
  DB 14; Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington
COUNTRY: USA
ZIP: 99104-702
ZIP: 99104-702
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STEET: 6500 Columbia Center, 701 Fifth Avenue
CITY: Seattle
100.0%; Score 1949; DB 14;
100.0%; Pred. No. 1e-145;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence.107, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355
                         Best Local Similarity 100.
Matches 391; Conservative
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  Query Match
Best Local
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                              241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG 180
                                                                                          LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                                                                                                   LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
                                                                                                                                                                                                                                                                                                               LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTOGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                    MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky, Yasir A.W.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: FLODRY disk
COMPUTER: Independatible
OPERATING SYSTEM: PC-COMPACIBLE
OPERATING SYSTEM: PC-COS/MS-DOS
CURRENT APPLICATION DATE:
RILING DATE: 10-Jul-2002
CLASSIFICATION NUMBER: US/10/193,002
FILING DATE: 0-Jul-2002
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION: CUNKNOWN>
RAPLICATION NUMBER: US/09/072,596
ATPLICATION NUMBER: US/09/072,596
ATPLICATION NUMBER: 05-MAY-1998
ATPLICATION NUMBER: 31 392
REGISTRATION NUMBER: 31 392
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REGISTRATION NUMBER: 31 392
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ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                       361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 102, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
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TELEPHONE: (206) 622-4900
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LENGTH: 391 amino acids
TYPE: amino acid
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APPLICANT: DILLOW, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Compos-Neto, Antonio
APPLICANT: Compos-Neto, Antonio
TITLE OF INVENTION: Ension Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: 014058-0090003
CURRENT APPLICATION NUMBER: US/09/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR PELING DATE: 1998-04-07
PRIOR PELING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 596
                                                                                                                                                                                                    61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
                                                                                                                                                                                                                                                                                                     121 LIATNILIGONTPAIAVNEAEYGEMWAQDAAANFGYAAATATATATLILPFEEAPEMTSAGG 180
                                                                                                                                                                                                                                                                                                                                                                                  241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
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                                                                                                             1 MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                     1 MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                 61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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    100.0%; Pred. No. 1e-145; ive 0; Mismatches 0; Indels
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; Patent No. US20020009459A1
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ORGANISM: Artificial Sequence
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                             391; Conservative
Best Local Similarity
Matches 391; Conserv
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APPLICANT: Skelky, Yasir; APPLICANT: Skelky, Yasir; APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a TITLE OF INVENTION: Leishmania Antigen; TITLE OF INVENTION: Leishmania Antigen; TITLE OF INVENTION UNBER: US/10/098,732A; CURRENT APPLICATION NUMBER: US/10/098,732A; CURRENT FILING DATE: 2001-04-29; PRIOR FILING DATE: 2001-03-13; NUMBER OF SEQ ID NOS: 80; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 391
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                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 1949; DB 14; Length 391; Best Local Similarity 100.0%; Pred. No. 1e-145; Matches 391; Conservative 0; Mismatches 0; Indels 0;
       REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                        TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 107:
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                                                                                                                                                     LENGTH: 391 amino acids
TYPE: amino acid
                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
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US-10-098-732A-14
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US-10-39-460-26
US-10-39-460-26
Publication No. US20030147911A1
GENERAL INFORMATION:
APPLICANT:
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APPLICANT:
Corisa Corporation Protiens of Mycobacterium tuberculosis Antigens
ITILE OF INVENTION:
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APPLICANT:
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APPLICATION NUMBER:
US/00/287,849
PRIOR APPLICATION NUMBER:
US/09/287,849
PRIOR APPLICATION NUMBER:
US/09/287,849
PRIOR FILING DATE:
1997-00-18
PRIOR FILING DATE:
1997-01-18
PRIOR FILING DATE:
1998-04-07
PRIOR APPLICATION NUMBER:
US/09/25,556
PRIOR APPLICATION NUMBER:
US/09/26,556
PRIOR APPLICATION NUMBER:
US/09/2019
PRIOR APPLICATION NUMBER:
US/09/2019
PRIOR FILING DATE:
1998-04-07
PRIOR FILING DATE:
1998-04-07
PRIOR PRIOR APPLICATION NUMBER:
US/09/2019
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      189 LIEGAAAVEEASDIAAANQLAMNVPQALQQLAQPIQGTTPSSKLGGLWKTVSPHRSPISN 248
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US-10-359-460-26
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Fublication No. US20040086523A1

Fublication No. US20040086523A1

APPLICANT: Skeiky, Yasir

APPLICANT: Reed, Steven

APPLICANT: Reed, Steven

APPLICANT: Coixa Corporation

ITLE REPERRACE: 014059-00970US

CURRENT APPLICATION NUMBER: US/09/886,349A

FILE REPERRACE: 2001-06-20

PRIOR PILING DATE: 2000-06-20

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PRIOR PILING DATE: 2001-06-20

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PATENTING DATE: 2010-02-01

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 20

LENGTH: 596
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UG-9-287-499-22

UG-9-287-499-22

Sequence 22, Application US/09287849

Patent No. US20020009459A1

FARBERL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: APPLICANT: AND ANTON:

APPLICANT: Campos-Neto, Mark

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Langer Fusion Protiens of Mycobacterium tuberculosis Antigens

TITLE OF INVENTION: Fusion Protiens

TITLE OF INVENTION: Pusion Protiens

CURRENT APPLICATION NUMBER: US/09/287,849

CURRENT FILING DATE: 1997-04-07

PRIOR FILING DATE: 1997-03-13

PRIOR APPLICATION NUMBER: US 09/025,197

PRIOR APPLICATION NUMBER: US 09/025,197

PRIOR APPLICATION NUMBER: US 09/025,566

PRIOR APPLICATION NUMBER: US 09/025,566

PRIOR APPLICATION NUMBER: US 09/223,040

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; Sequence 22, Application US/10359460
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APPLICANT: Glacian, Jeffrey
APPLICANT: Glacian, Jeffrey
APPLICANT: Glacian, Jeffrey
APPLICANT: Glacian, Jeffrey
APPLICANT: Glacian, Jeffrey
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising of TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising of TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION: Leishmania Antigen
TITLE OF INVENTION NUMBER: US 100,098,732A
CURRENT APPLICATION NUMBER: US 60/275,837
PRIOR PRILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 20
LENGTH: 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1949; DB 14; Length 596; 100.0%; Pred. No. 1.8e-145; cive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                        361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                 369 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-10-098-732A-20
; Sequence 20, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 391, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-886-349A-18
                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 723
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              GENERAL INFORMATION:
APPLICANT: Reed Steven G.
APPLICANT: Reed Steven G.
APPLICANT: Steriky, Yasir A.W.
APPLICANT: Steriky, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-0090200S
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT APPLICATION NUMBER: US/025026
FILE REFERENCE: 014058-0090200S
CURRENT APPLICATION NUMBER: US/025,287,849
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR PELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
MS-10-359-460-22
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ORGANISM: Artificial Sequence
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Best Local
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Sequence 2, Application US/10369983; Publication No. US20030235593A1; GENERAL INFORMATION:

US-10-369-983-2

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301 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 MVDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLIVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Red, Steven
APPLICANT: Red, Steven
APPLICANT: Red, Steven
APPLICANT: Coriver Corporation
APPLICANT: Coriver Corporation
APPLICANT: Coriver Corporation
APPLICANT: Coriver Corporation
APPLICANTON: UNGO Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT FILING DATE: 2003-02-18
PRIOR PRILING DATE: 2003-02-18
PRIOR PLING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 2.1
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Publication No. US20040086523A1
Publication No. US20040086523A1
APPLICANT Seed, Steven
APPLICANT: Reed, Steven
APPLICANT: Adearson, Mark
APPLICANT: Adearson, Mark
APPLICANT: Orixa, Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
CURRENT.APPLICATION UNBER: US/09/886,349A
CURRENT.FILING DATE: 2001-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:mutated CTHER INFORMATION: MTB32-MTB39F fusion protein (MTB32MutSA) US-10-369-983-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
100.0%; Score 1949; DB 15; Length
Best Local Similarity 100.0%; Pred. No. 2.3e-145;
Matches 391; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
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LLEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
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                        1 MVDFGALPPEINSARMYAGPGSASIVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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US.10-369-281-21
iS-10-369-281-21
iS-10-369-281-21
iS-10-369-281-21
iS-20-362-31, Application US/10369983
j Publication No. US20030235593A1
j GENERAL INFORMATION:
j APPLICANT: Skeiky, Yasir
j APPLICANT: Skeiky, Yasir
j APPLICANT: Guderian, Jeff
j APPLICANT: Reed, Steven
j APPLICANT: Corisa Corporation
j TILLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
j FILE REPREMENCE: 04608-009081US
j CURRENT APPLICATION NUMBER: US/10/369,983
j CURRENT FILING DATE: 2003-02-18
j PRIOR PILING DATE: 2003-02-15
j NUMBER OF SEQ ID NOS: 22
j SOGFWARE: Patentin Ver. 2.1
j SEQ ID NO 21
i LENGTH: 729
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US-10-369-983-21
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100.0%; Score 1949; DB 15; Length
Best Local Similarity 100.0%; Pred. No. 2.4e-145;
Matches 391; Conservative 0; Mismatches 0; Indels
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US-10-098-732A-18
is Sequence 18, Application US/10098732A
is Publication No. US20030175294A1
is GENERAL INFORMATION:
is APPLICANT: Skeiky, Yasir
is APPLICANT: Brannon, Mark
is APPLICANT: Guderian, Jeffrey
is APPLICANT: Coriza Corporation
if TITLE OF INVENTION: Heterologue Fusion Protein Constructs Comprising a
rITLE OF INVENTION: Leishmania Antigen
is TITLE OF INVENTION NUMBER: US/10/098,732A
is CURRENT APPLICATION NUMBER: US 60/275,837
is PRIOR FILING DATE: 2003-04-29
is PRIOR PILING DATE: 2001-03-13
is NUMBER OF SEQ ID NOS: 80
is SEQ ID NOS: 80
is SEQ ID NO 18
is LENGTH: 729
                                                                                                                                                                                                                                                                                142 MYDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIG
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COTHER INFORMATION: Description of Artificial Sequence:MTB72FMutSA; OTHER INFORMATION: (Ral2-TbH9-Ra35MutSA)
                                                                              FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:MTB72FMutSA;

OTHER INFORMATION: (Ral2-TbHp-Ra35MutSA)

18-09-886-349A-18
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Best Local Similarity 100.0%; Pred. No. 2.4e-145;
Matches 391; Conservative 0; Mismatches 0; Indels
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    SEQ ID NO 18
LENGTH: 729
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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MVSMANNHMSMINSGVSMINILSSMLKGFAPAAAAQAVQIAAQNGVRAMSSLGSSLGSSG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                        | Sequence 22, Application US/10369983
| Publication No. US20030235593A1
| Publication No. US20030235593A1
| GENERAL INFORMATION: Skeiky, Yasir
| APPLICANT: Guderian, Jeff
| APPLICANT: Guderian, Jeff
| APPLICANT: Guderian, Jeff
| APPLICANT: Corixa Corporation
| TILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
| TILE REFERENCE: 014058-0090810.
| FILE REFERENCE: 014058-0090810.
| CURRENT APPLICATION NUMBER: US/10/369,983
| CURRENT APPLICATION NUMBER: US/0/357,351
| PRIOR APPLICATION NUMBER: US 60/357,351
| RIOR PILING DATE: 2002-02-15
| NUMBER OF SEQ ID NOS: 22
| SOFTWARE: PatentIn Ver: 2.1
| SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 1949; DB 15; Length 729; Best Local Similarity 100.0%; Pred. No. 2.4e-145; Matches 391; Conservative 0; Mismatches 0; Indels 0;
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OTHER INFORMATION: Description of Artificial Sequence:mutated
OTHER INFORMATION: MTB72FMutSA (Mtb72f-mutSA)
US-10-369-983-22
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ORGANISM: Artificial Sequence
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OM protein - protein search, using sw model

June 30, 2004, 16:43:31; Search time 10.2189 Seconds (without alignments) 3680.509 Million cell updates/sec Run on:

US-09-597-796C-8 1949 1 MVDFGALPPEINSARMYAGP......SGVLRVPPRPYVMPHSPAAG 391 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	е РРЕ	PPE	PPE (PPE	probable PPE prote	PPE	PPE	ly pr	BPE :	PPE	PPE	PPE	PPE	PPE	PPE	PPE	e PPE	PPE	a	PPE	PPE	e PPE	PPE		PPE	PPE prot	PPE prot	PPE prot	PPE
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361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391

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443 441 439.5	4 4 2 9 . 5 . 5 . 5 . 5 . 5 . 5 . 5 . 5 . 5 .	423.5 422.5 418	415.5 415 414.5	412 412 409.5
330	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	9 7 8 9	4 4 4 0 4 0	4 4 4 6 4 7

ALIGNMENTS

	RESULT 1	
	probable	B/0808 Probable PPE protein - Mycobacterium tuberculosis (strain H37RV) Propagion: Mochantorium tuberculosis
	C; Date: 1	Cipecies: In-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
	C;Accessi R;Cole, S ; Connor, Rajandrea	
	Nature 393, A;Authors: (A;Title: Dec A;Reference	Nature 393, 577-544, 1998 A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A,Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome : A,Reference number: A70500; MUID:98295987; PMID:9634230
	A;Accessi A;Status: A;Molecul	A,Accession: B70608 A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
	A, Residues: A, Cross-ref. A, Experimen C, Genetics: A, Gene: PPE	A,Residues: 1-391 <ccl> A,Cross-references: GB:Z93777, GB:AL123456, NID:g3261726, PIDN:CAB07839.1, PID:e311073; I A,Cross-references: GB:Z93777, GB:AL123456, NID:g3261726, PIDN:CAB07839.1, PID:e311073; I C,Genetics: A,Gene: PPE</ccl>
	Query Match Best Local Sim Matches 391;	Query Match Best Local Similarity 100.0%; Pred. No. 3.5e-108; Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	ò	1 NVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 60
	DÞ	1 NVDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIG 60
	È	61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAXETAYGLTVPPPVIAENTAELMI 120
	qq	61 SSAGLMVAAASPYVAMMSVTAGQABLTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
, · · · · ·	ò	121 LIATNILGONTFALAVNEAEYGEWAQDAAMFGYAAATATATLIPFEEAPEMTSAGG 180
	qq	121 ilatniligontpalavneabygemmaqdaaampgyaaatatatatilippeeapemisagg 180
· -	δλ	181 LIEGAAAVEEASDTAAANQLMNNVPQALQQFIQQTTESSKLGGLWKTVSPHRSPISN 240
· · ·	QQ Q	181 LIEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
	ò	241 WVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
	Dp	241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
111.12.0	ò	301 LGGGVAANIGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
.	qq	301 LGGGGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360

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Gaps

9 9 120 120 180 240 240 296 299

g

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A;Residues: 1-393 cCOL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17711.1; PID:e1254600
A;Experimental source: strain H37Rv
A,Molecule type: DNA
A,Residues: 1-393 <COL>
A,Residues: 1-393 <COL>
A,COSS-references: GB:Z95390; GB:AL123456; NID:g3261766; PIDN:CAB08702.1; PID:e316074; A,Experimental source: strain H37Rv
C,Genetics:
A,Gene: PPE
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-dul-1998 #sequence_revision 17-dul-1998 #text_change 22-Oct-1999
C;Accession: G70529
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S. Radiancean M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
NAIthoris: Sqares, R.; Sulston, J.E.; Taylor, K.; Whithehead, S.; Barrell, B.G.
A;Anthoris: Sqares, R.; Sulston, J.E.; Taylor, K.; Whithehead, S.; Barrell, B.G.
A;Anthoris: Sqares, R.; Sulston, J.E.; Taylor, K.; Whithehead, S.; Barrell, B.G.
A;Anthoris: Sqares, R.; Squares, R.; Shallon, S.; Barrell, B.G.
A;Anthoris: Sqares, R.; Squares, R.; Mycobacterium tuberculosis from the complete genome A;Reference number: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSSGLGGCVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVDFGALPPEINSARMYAGPGSASLVAAAKMMDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SSAGLMAAAASPYVAMMSVTAGQAQLTAAQVRVAAAAYETAYRLTVPPPVIAENRTELMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 VSSIANNHMSMMGTGVSMTNTLHSMLKGLAP-AAAQAVETAAENGVWAMSSLGSQLGSSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 LLEQAVAVEEAIDTAAANQLMNNVPQALQQLAQPAQGVVPSSKLGGLWTAVSPHLSPLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL
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                                                                                                                                                                                                                                                                            Query Match 81.2%; Score 1583; DB 2; Best Local Similarity 81.5%; Pred. No. 1.5e-86; Matches 322; Conservative 20; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
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C;Species: Mycobacterium tuberculosis
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: C70568
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobaccerium tuberculosis from the complete genome A;Reference number: A70500; MuID:98295987; PMID:9634230
A;Accession: C70568
A;Atatus: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.0%; Score 1656.5; DB 2; Length
85.1%; Pred. No. 6.7e-91;
ive 18; Mismatches 34; Indels
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    GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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Best Local Similarity 85.1%
Matches 338; Conservative
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Probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: H70931
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Rochor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome s A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Residues: 1-403 cCOL-
A;Cross-references: GB:AL022021; GB:AL123456; NID:93250699; PIDN:CAA17728.1; PID:e1254618
A;Gene: PPE
A;Gene: PPE
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 WLDKLWALLDPN-----SNFWNTIASSGLFLPSNTIAPFLGLLGGVAAADAAGDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 LGEATSG-----GLGGALVAPLGSAGGLGGTVAAGLGNAATVGTLSVPPSWTAAAPLASP
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AAEAPGALFGEMALSSLAGRALAGTAVRSGAGAARV 388
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Matches 181; Conservative
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C.Species: Mycobacterium tuberculosis
C.Date: 17-Uul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C.Accession: A70932
R.Jocle. S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
A.Accession: A70932
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-409 <COL>
A.Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17729.1; PID:e125461
A; Experimental source: strain H37RV
C;Genetics:
A,Gene: PPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 RSPISNMVSMANNHMSMTNSGVS-----MTNTLSSMLKGFAPAAAQAVQTAAQNGVRAM 289
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                                                                                                                                          ----TVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAA
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                                                                                                                                                                                                                                                                                                                                                                             342 SLISAAERGPGOMLGGLPVGOMGARAGGGLSGVLRVPPRPYVMPHSPAAG
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A;Molecule type: DNA
A;Residuss: 1-408 <COL>
A;Cross.references: GB:Z74024; GB:AL123456; NID:g3250700; PIDN:CAA98377.1; PID:e1301025;
A;Expenimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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                                                                                   II MFDPAALSPETNSTRMYLGPGSSPILTAAAAWVVLAKELTAAAQGLQSAVEAL-LTTFEG
                                                1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                           LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPENTSAGG
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41.8%; Pred. No. 1.1e-34;
tive 47; Mismatches 134;
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70931
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: DNA
A;Molecule type: DNA
A;Residues: 1-423 <COL>
A;Cross-references: GB:AL022021; GB:AL123456; NID:93250699; PIDN:CAA17722.1; PID:e125461
C;Genetics:
A;Gene: PPE
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R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R; Davies, R.M.; Davlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
Ajathors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
Ajathors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
Ajathors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
Ajathors: Pareliminary
Ajathors: preliminary
Ajathors: Preliminary
Ajathors: DNA
Ajathors: L421 cSTO>
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PPE-family protein [imported] - Mycobacterium leprae
PPE-family protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Date: 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 TQNGQGVSALLGKIGGKPITGALAPLAEFALHTPILGSEGLGGGSVSAGIGRAGLVGKLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 IATNIFGONTPAIMMTEAQYMEMWAQDAAAWYGYAGSSATA-SRWTAFTEPPQTINHGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 LEQAAAVEEASDTAAAN-----QLMMNVPQALQQLAQPT----QGTTP-----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 TFLGG--AVTGPYTFP-----GVLPPSGVPYLLGIQSVL-----V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80;
                                                                                                                                                                                                                                                                                                                                                                                                  37.8%; Score 736; DB 2; Length 423; ilarity 41.8%; Pred. No. 1.8e-36; Conservative 50; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---HPIGSAAAPAVG 400
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Best Local S
Matches 182
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Length 408;

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122 IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGL

VATNFFGONTPALAATEAQYAEMWAQDAAMYAYAGSAAIAT-ELTPFTAAPVTTSPAAL

121 182

8,

34; Gaps

Query Match
37.5%; Score 731; DB 2; Length 421;
Best Local Similarity 41.1%; Pred. No. 3.5e-36;
Matches 174; Conservative 55; Mismatches 160; Indels 3

A; Gene: ML1182

à 엄 LEQAAA-----VEEASDTAAANQLMNN-----VP--QALQQ-LAQPTQGTTPSSKL--- 224

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
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C;Species: Mycobacterium tuberculosis
C;Dates: 17-041-1998 #sequence_revision 17-041-1998 #text_change 22-Oct-1999
C;Accesion: B7025
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, M.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Altle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:9829587; PMID:9634230
A;Accession: B70625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P--ISNMVSMANNHMS-MTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLG 293
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                                                                                                       240 RLLGISYFDEGL------LQFEASLAQQAIPGTPGGAG--DSGSSVLDSWGPTIFA
                                                                                                                                                                                                               -- SGLGGGVAANLGRAASVGSLS
                                                                                                                                                                                                                                                                                                                               339 VPPDWAARARWANPAAWRLPGDDVTALRGTAENA---LLRGFPWASAGQSTGGGF--VHK
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                                                                             -----GGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAA
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36.0%; Score 702; DB 2; Length 391;
Best Local Similarity 42.3%; Pred. No. 1.6e-34;
Matches 166; Conservative 62; Mismatches 150; Indels
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                                                                                                                                                                               QAVQTAAQNGVRAMSSL--GSSLGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                  394 YGFRLAVMORPPFÄG 408
                                                                                                                                                                                                                                                                                                                                                                               377 VPPRPYVMPHSPAAG 391
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: Pro560
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Ritle: Deofiphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MUD:98295987; PMID:9634230
A;Reference number: A70500; MUD:98295987; PMID:9634230
A;Retures preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-413 <COL>
A;Cross-references: GB:Z95436; GB:AL123456; NID:g3261770; PIDN:CAB08826.1; PID:e316565; I
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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C70931
Cyobable PPE protein - Mycobacterium tuberculosis (strain H37RV)
Cyobable PPE protein - Mycobacterium tuberculosis
Cybate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
Cybate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
Cybate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
Cybate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
Cybate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAA---AAQAVOT---
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A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Accession: C70931 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule rype: DNA A; MOlecule rype: DNA A; PROSECTION APPROREMENTA A; APPRORE	61 61
A/RESTRUCES: TT. 403 COLD. A/Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17723.1; PID:e125461 A/Experimental source: strain H37Rv C;Genetics: A/Gene: PPE	INTINITION FAITANNESS TO SEMINAQUE MANICIPALIS IN THE FEBRE STORY VAINIFGONTAAIAATEAEYGEMWAQDIWAMFGYASSSATA-SKLIPFTAPPOTINPSGL LEGAAAVEEAS
Query Match 35.3%; Score 688.5; DB 2; Length 463; Best Local Similarity 42.8%; Pred. No. 1.3e-33; Matches 174; Conservative 48; Mismatches 136; Indels 49; Gaps 11;	Db 180 AGQAAATGQATALASGTNAVTTALSSAAQFPFDIIPTLLQGLATLSTQYTQLMGQLI 237 Qy 228WKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQ 276
CY 2 VDFGALPPEINSARMYAGPGSASLVAAAOMMDSVASDLFSAASAFQSVVWGLIVGSWIGS 61	Db 238 NAIFGPTGATTYQNVFVTAANVTKFSTWANDAWSAPNLGMTEFKVFWQPPPAPE 291 Qy 277 AVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAASVGSLSVPQAWAAANQA 331
QY 62 SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121	in Σ
QY 122 IATNLLGQNTPAIAVNEAEYGEMWAQDAAANFGYAAATATATATLLPFEEAPEMTSAGGL 181	Db 342 RLVANTLPATSLAAAPATQIPANLLGQMALGSMTGGAL 379
OY 182 LEQABANEEASDTABANQLMNNVPQALQQLAQPTQCTTPSSKLGGLWKTVSPHRSPI- 238	RESULT 14 A70646 probable PPB protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis
QY 239SNMVSMANNHMSMINSGVSMINTLSSMLKGFAPAAAAQAVQTAAQNGVRA 286 Db 236 NSMLGLGFAESKAVLPANDTVISTIFGMVQFQKFFNPVTPFNPDLIPK 283	C; Date: 1UL-1998 #Sequence_revision 1/-ULL-1998 #textchange 24-Oct_1999 C; Accession: A70646 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Qy 289 MSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPL 340 Db 284 -SALGAGLGLRSAISSGLGSTAPAISAGASQAGSVGGMSVPPSWAAATPAIRTVAAVFSS 342	Rajandream; M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome &
OY 341 TSLTSAAERGPGOMLGGLPVGOMGARAGGGLSGVLRV 377	A.Reference number: A70500; MUID:98295987; PMID:9634230 A.Accession: A70646 A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Molecule: type: DNA
strain H37RV)	A; Residues: 1-380 <cud.> A; Cross-references: GB:Z83867; GB:AL123456; NID:g3261695; PIDN:CAB06278.1; PID:e291015; F A; Experimental source: strain H37Rv C; Genetics: A; Gene PPE</cud.>
ge 22-Oct-1999	Query Match 34.6%; Score 675; DB 2; Length 380; Best Local Similarity 43.1%; Pred. No. 6.2e-33;
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.	Matches 172; Conservative 56; Mismatches 143; Indels 28; Gaps 12; Qy 2 VDFGALPPEINSARMYAGPGSASIVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS 61
Nature 533, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230	Db 1 MDFALLPPEVNSARMYIGPGAGSILAAAGGWDSLAABLATTABAYGSVLSGLAALHWRGP 60 OY 62 SAGLMVAAABYVAGQAELTAAQVRVAAAAYFTAYGLTVPPPVIABNRAELMIL 121
A;Accession: B70932 A;Etatus: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA	DD 61 AAESMAVTAAPYIGWLYTTAEKTQQTAIQARAAALAFEQAYAMTLPPPVVAANRIGLLAL 120
A;Residues: 1-468 <col/> A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17730.1; PID:e125462 A;Experimental source: strain H37Rv	OY 122 IATWILGONTPAIAVNEAEYGEMMAQDAAAMFGYAAATATATLIPFEEAPEMTSAGGL 181
3E 08. Octobe 603 E. DD 3.	CY 182 LEQAAAVEEASDTAAANQLMUNVPQALQQLAQPTCGTTPSSKLGGLWKTVSPHRSPI 238
Similarity 40.9%; Pred. No. 2.9e-33; Fengun 4; Conservative 59; Mismatches 125; Indels	239 SINW'SM ANNHAMINSGVSMITKSSMIKGFRPAAAAQAVOTAAQNGVRAMSSIGSSI
QY 2 VDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIGS 61	GIGELUSA ANQAVTPAARALP

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Decies: Mycobacterium tuberculosis
C;Decies: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G70881
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Aterence number: A70500; WUDD: 98295997; FMID: 9634230
A;Accession: G70881
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290 GAASVGNTVLASVGRANSIGQLSVPPSWAAPSTRPVSALSPAGLTTLPGTDVAEHGMPG- 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.3%; Score 668.5; DB 2; Length 394; 40.8%; Pred. No. 1.6e-32; tive 61; Mismatches 156; Indels 17
                                                                                                                                                                349 -VPGVPV-----AAGRASGVLPRYGVRLTVMAHPPAAG 380
                                                                                           354 MLGGLPVGQMGARAGGGLSGVL-RVPPRPYVMPHSPAAG 391
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Job time : 11.2189 secs
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Best Local Similarity 40.85
Matches 161; Conservative
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 30, 2004, 16:42:21; Search time 6.3659 Seconds (without alignments) 3198.204 Million cell updates/sec Run on:

US-09-597-796C-8 1949 1 MVDFGALPPEINSARMYAGP.....SGVLRVPPRPYVMPHSPAAG 391 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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                                                                                                                                                                                                            1,
                                                                                                                                                       DB 1; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                 85.0%; Score 1656.5; DB 1; Length
85.1%; Pred. No. 1.3e-89;
ive 18; Mismatches 34; Indels
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15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
14-Ppothetical PPE-family protein Rv2892c/MT2959/Mb2916c.
RV2892C OR MT2959 OR MTCY274.23C OR MB2916C.
Mycobacterium tuberculosis, and
                                                           158 159 TA -> AT (IN REF. 2).
396 AA; 40015 MW; 6AFAE0D7B5F668D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLPVGQMGARAG -- GGLSGVLRVPPRPYVMPHSPAAG 391
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NCBI_TaxID=1773, 1765;
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                               Hypothetical protein; Complete proteome,
CONFLICT 158 159 TA -> AT (1
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Matches 338; Conservative
Pfam; PF00823; PPE; 1.
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                                                                                     SEQUENCE
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DT 10-0CT-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IATNILIGONIPALAVNEAEYGEMWAQDAAAMFGYAAATATATILLEFEEAPEMTSAGGL 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R., Yr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72;
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41.8%; Pred. No. 2.7e-34;
ive 47; Mismatches 134; Indels
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EMEL; BX248344; CAD96603.1; -
EMEL; BX248344; CAD96603.1; -
ETGR; G70925; G70925; -
TIGR; MT2959; -
TUBErCULIST; RV2892c; -
TUBERCULIST; RV2892c; -
FAMFORD PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Transmembrane; COTRANSMEM 56 76 POTENTIAL.
                                                                                                                          ooratory strains.";
Bacteriol. 184:5479-5490(2002)
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46021 MW; EE64828BF09FA551 CRC64;

463 AA;

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SEQUENCE
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Y442_MYCTU
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SPECIES=M tuberculosis; STRAIN-CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weiden L.A., Khouri H., Gill J., Mikula A., Blishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES—M. bovis; STRAIN=AF2122/97; Medina N., Mansoor H., Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barreil B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100;7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=M.tuberculosis, STRAIN=H37Rv;

MEDLINE=99295987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Badcock K., Devlin K., Feltwell T., Gentles S., Haminn N., Holroyd E.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

Sulters S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence.";
                                                                                                                                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1802/MT1851/Mb1830.
Mycobacterium tuberculosis, and
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InterPro; IPR000030; Microbac_PPE.
Pfam, PF00823; PPE; 1.
Hypothetical protein; Complete proteome.
COMPLICT 401 401 S -> L (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome sequence
Nature 393:537-544(1998)
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                    Mycobacterium bovis.
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                                                                                                                                                                                                                                                                                   182 LEGAAAVEEASDTAAANQLANNVPQALQQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI- 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 MSSLGSSLG----SSGLGG----GVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPL 340
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                                                                                                                                                                                                                                          62 SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd P., Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Balston J.S., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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J. Bacteriol. 169:1080-1088 (1987).
      Length
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCB1_TaxID=1773;
; Score 688.5; DB 1;
; Pred. No. 2.8e-33;
48; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7442 MYCTU STANDARD; PRT; 487 AA. P426TI; 05372; 1.05372; 1.05772; 1.0507-2001 (Rel. 40, Last sequence update) 110-007-2003 (Rel. 42, Last annotation update) 14090chetical PPB-family protein Rv0442c/MT0458 RV0442c OR MT0458 OR MTV037.06C.
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MEDLINE=87137260; PubMed=3029018;
      35.3%;
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STRAIN=CDC 1551 / Oshkosh;
                                                                  174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AAMMAVATQYLAWISTAAAQAEQAAAQAMAIATAFEAALAATVQPAVVAANRGINQILAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 INLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAG---- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 KNGQINLGFGNTGSGNIGNNNIGNNNIGSGNTGTGNIGSGNTGSGNLGLGNLGDGNIGFG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 KTVS------PHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTSLTSAAERGPGQM-----LGGLPVGQMGARAG--GGLSGVLR--VPPRPYVMPHSPAA 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Gaps
           Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 NTGSGNIGFGITGDHQMGFGGFNSGSGN-IGFGNSGTGNVGLFNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                      22.8%; Score 444; DB 1; Length 48 32.1%; Pred. No. 4.8e-19; ive 48; Mismatches 180; Indels
                                                                                             J. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                          Complete proteome.

E -> K (IN REF. 2).

I -> T (IN REF. 1).

G -> GANNIG (IN REF. 1).

7247 MW, 97234D5B316C8C7F CRC64;
                                                                                                                                                                                                entities requires a license agreement ((or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                           InterPro; IPR000030; Microbac PPE.
InterPro; IPR002899; Mycobac Dentapep.
Pfam; PF01469; Pentapeptide_2; 5.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                      EMBL; M15467; AAA88235.1; ALT_INIT.
MEDLINE=22206494; PubMed=12218036
                                                                                                                                                                                                                                                EMBL; AL021932; CAA17399.1; -. EMBL; AE006948; AAK44681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                              487 AA; 47247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 135; Conservative
                                                                                                                                                                                                                                                                                   TIGR; MT0458; -.
Tuberculist; Rv0442c; -
                                                                                                                                                                                                                                                                                                                                                                                                  211
                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                    laboratory strains.";
                                                                                                                                                                                                                                                                          PIR; C70830; C70830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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MEDLINE=22206449; Pubmed=1218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delbher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98295987; PubMed=9634230; Cole S.T., Erosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole Gordon S.V., Eighmeier K., Gas S., Barry C.E. III. Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hernsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oldver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Pociphering the biology of Mycobacterium tuberculosis from the
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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4 X 10 AA APPROXIMATE REPEATS.
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                                                                                          OLOCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
14)-OCT-2003 (Rel. 42, Last annotation update)
17)-OCT-2003 (Rel. 42, Last annotation update)
17)-OCT-2003 (Rel. 42)
18)-OCH-2003 (Rel. 42)
18)-OCH-2003 (Rel. 42)
18)-OCT-2003 (Rel. 42)
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Tuberculist, Rv0878c, -.
InterPro, IRR000303, Microbac_PPE.
InterPro, IRR002393, Mycobac_Dentapep.
Pfam, PF0J469, Pentapeptide_2, 4.
Pfam, PF00823, PPE, 1.
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EMBL, AE006977; AAK45143.1; ALT_INIT.
PIR; C70780; C70780.
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                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
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                                                                                                       119 MILIATNILIGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSA 178
                                                                                                                                                         238
                                                                                                                                                                                  208
                                                                                                                                                                                                            278
                                                                                                                                                                                                                                     268
                                                                                                                                                                                                                                                              279 QTAAQNGVRAMSSLGS-SLGSSGLGGGVAA--NLGRAASVGSLSVPQAWAAANQAVTPAA 335
                          9
                                                                                                                                                                                                                              209 GNFLGIGNIGNNNVGSGNTGDYNFGIGNIGNANLGNGNIGNANLGSGNAGFFNFGNGNDG
               SNWV---SMANNHMSMTNSG-----VSMTN----TLSSMLKGFAPAAAAQAV
                                                                                                                                                                                                                                                                                         ---MGNSGD----
                                                   59 IGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAEL
                                                                                                                                                         179 GGLLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Obikosh;
MEDLINE=CDC 1551 / Obikosh;
MEDLINE=CD2206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Peterson J., White O., Eisen J.A., Ermolaeva M., Salzberg S.L., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weinden J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=H37RV;
MEDLINE=9825987; PubMed=9634230;
MEDLINE=9825987; PubMed=9634230;
Gordon S.V., Eiglmeier R., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., Mchean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                   --LLSVLPPVVTAAPAGAV----GVPAA---LAIPALGV---ENIG-----
  VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.

    SIMILARITY: Belongs to the mycobacterial PPE family.

                                                                                                                                                                                                                                                                                       269 NINFGSGNAGFLNIGSGNEGSGNLGFGNAGDDNTG-----
                                                                                                                                                                                                                                                                                                                  336 RALPLISLISAAERGPGQMLGGL--PVGQMGARAGGGLSG 373
                                                                                                                                                                                                                                                                                                                                   01-00T-1996 (Rel. 34, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
10-00T-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1548c/MT1599.
                                                                                                                                                                                                                                                                                                                                                                                                              678 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 393:537-544 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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Thompson J.K., Hussain R., Stoker N.G.;
"Sequence and immunological characterization of a serine-rich antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AVIIAGFPFLDLGNVTIGGFNLASGNLGLGNLGS-----FNPGSANTGSVNLGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 IATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLLPFBEAPEMTSAGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Mismatches 140; Indels
                                                                                                                                                                                                                                                        Tuberculist; Rv1548c; -.
Interpro; IRR00030; Midrobac PPE.
Interpro; IRR002999; Mycobac pentapep.
Interpro; PR002999; Mycobac pentapep.
Interpro; PR01469; Pentapeptide 2; 11.
Pfam; PF00482; PPE; 1.
Hypothetical protein; Transmembrane; Complete proteome.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      558 D -> G (IN REF. 2).
66736 MW; 209F1593D52533A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRA MYCLE STANDARD; PRT; 408 AA. 207297; 007297; 01-NOV-1995 (Rel. 32, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Serine-rich antigen (25L) (45 kDa protein). Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 SLGSSLGSSGLGGGVA--ANLGRAASVGSLSV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 LGGGNLGSYNLGSGNTGDTNFG-GGNTGNLNV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 418;
Pred. No. 2
                                                                                                                                                        EMBL; Z74020; CAA98335.1; -.
EMBL, AE007026; AAK45866.1; ALT_INIT.
PIR; A70762; A70762.
TIGR; MT1599; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTI
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Infect. Immun. 61:2145-2153(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.4%;
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258 2
678 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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                                                                                                                             262 LSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAAN----LGRAASVG 316
                                                                                                                                                                   287. ASSIM----PIVASQVTETLGRSQV-AVERMIQSISSTAVSVDVAASKVVAGVGQAVSVG 341
214 ----PTQ-----GTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNT 261
                                                                                                                                                                                                                                                    317 SLSVPQAWAAANQAVTPAARALP--LTSLTSAAERGPGOMLGGLPVGQMGARAGGGLSGV 374
                                                                                                                                                                                                                                                                                                                     ---VSGPLEGV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=9825987; PubMed=9634230; Cole S.T., Erosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elgilmeler K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Bromn D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hallin N., Holroyd S., Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares R., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Squares R., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                             ---DSIISSASASLLTTNS--ISSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 184:5479-5490(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
HVDOCHETICAL PPE-family protein Rv0096/MT0105.
RV0096 OR MT0105 OR MTCY251.15.
                                                                                                                                                                                                                                                                                                342 ALRVPENWATASOPVMATAHSVPAGCSAITTA---
                                                         240 PFGTPSÓSSOSNDLSATSLTQQLGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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STRAIN-CDC 1551 / Oshkosh;
MEDLINE-22206494; PubMed-12218036;
                                                                                                                                                                                                                                                                                                                                                                                  375 LRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                               382 TO--PAEEVLTASVAGG 396
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EMBL; AE006922; AAK44327.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
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TIGR; MT0105; -.
Tuberculist; Rv0096; -.
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Q10892;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                                                           Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Monle S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutherford K.M., Steyens S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87; Gaps
                       Rinke de Wit T.F., Clark-Curtiss J.E., Abebe F., Kolkon A.H.J.,
Jonson A.A.M., Thole J.E.R.;
"A Mycobacterium leprae-specific gene encoding an immunologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%; Score 364.5; DB 1; Length 408; 26.3%; Pred. No. 1.7e-14;
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2 X 6 AA REPEATS OF S-V-A-Q-S-E.
1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
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S -> L (IN REF. 2).
H -> D (IN REF. 2).
P -> L (IN REF. 2).
SCOC2BEODGE6A9D8 CRC64;
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                                                                                                                                                                                                                                                                                   MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
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Pfam; PF00823; PPE; 1.
                                                                                                                      recognized 45 kDa protein.";
Mol. Microbiol. 10:829-838(1993).
MEDLINE=95020554; PubMed=7934845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42466 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, U00015; AAC43220.1; -.
EMBL, X68431; CAA48480.1; -.
EMBL, Z21952; CAA79950.1; -.
EMBL, Z97179; CAB09938.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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132
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408 AA;
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                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen; Repeat;
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                                                                                                                                                                                    [3]
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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REPEAT
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EMBL; AL021287; CAA16103.1; -.
EMBL; AE007129; AAK47427.1; ALT_SEQ.
EMBL, AE007129; AAK47430.1; ALT_SEQ.
EMBL; X59271; CAA41961.1; ALT_FRAME.
PIR; E70857; E70857.
                                                                                                                                  Bacteriol. 184:5479-5490(2002)
                                                                                                                                                         SEQUENCE OF 160-374 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 28.0
Matches 115; Conservative
Nature 393:537-544(1998)
                                                                                                                           laboratory strains.";
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                                                                                                                                                                                                                                       66 MVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATN 125
                                                                                                                                                                                                                                                      62 YVAAHGPYLAWLEQTAINSAVTAAQHVAAAAAYCSALAAMPTPABLAANHAIHGVLIATN 121
                                                                                                                                                                                                                                                                                     126 LLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQA 185
                                                                                                                                                                                                                                                                                                  122 FFGINTVPIALNEADYVRWHQAADIWAAYQAVADAATVAVPSTQPAPPIRAPGG---- 176
                                                                                                                                                                                                                                                                                                                                              ---GGLW------KTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLK----GF 269
                                                                                                                                                                                                                                                                                                                                                                                                    275
                                                                                                                                                                                                                                                                                                                                                                                                                          270 APAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQ 329
                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                  19
                                                                                                                                                                                                           230 QLYDFLWYPYYASYGLLLLPFFTP------TLSALTALSALTHLUNLPPAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                            6 ALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGL
                                                                                                                                                                                                                                                                                                                                  186 AAVEEASDI-----AAANQLMNNVPQALQQLAQPTQ------GTTPSSKL-----
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=H37Rv;

MEDLINE=98295987; PubMed=9634230;

MEDLINE=98295987; PubMed=9634230;

Cole S.T., Brosch R., Farkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Badcock K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.

Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

Sultter S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                        93;
                                                                                                                                                ; Score 324.5; DB 1; Length 463;
; Pred. No. 4e-12;
54; Mismatches 144; Indels 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 AVTPAARALPLISLISAAERGPG---QMLGGLPVG-QMGARAG 368
                           proteome
                                                                                                                POTENTIAL.
42D9D66A033D0DD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P31500; 053265;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv3018c/MT3098/MT3101.
RV3018C OR MT3098/MT3101 OR MTV012.32C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
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                                     POTENTIAL.
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                                                                                          POTENTIAL. POTENTIAL.
 InterPro; IPR000030; Microbac_PPB.
Pfam; PF00823; PPB; 1.
Hypothetical protein; Transmembrane;
                                                                                                                            46894 MW;
                                                                                                                                                   16.6%;
27.8%;
                                                                                                                                            Query Match
Best Local Similarity 27.85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                     1112
1112
2116
216
276
276
323
313
419
463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1773;
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TRANSMEM
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reductase.
-!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 294; 337 and 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 AAVEEASDTAAAN------QLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAASV-GSLSVPQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 --ANEASNAVAAATITPFFWHEIVOFLEETFAAYDOYLSALLSELPA--VAWVWFQLFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 MVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATN
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STRAIN=CDC 1551 / Oshkosh;

MEDINE-2206494; PubMed=12218036;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Braft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,

Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;

"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                        62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.6%; Score 324; DB 1; Length 43 28.0%; Pred. No. 4e-12; ive 56; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; MT3109; -.
TIGR; MT3101; -.
TIGR; MT3101; -.
Tuberculist; Rv3018c; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 434 AA; 43029 MW; 41D673C4BD389DD6 CRC64;
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Length 435;

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DB 1;
Query Match
16.5%; Score 321.5; DB 1;
Best Local Similarity 26.5%; Pred. No. 5.6e-12;
Matches 115; Conservative 53; Mismatches 159;
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10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv3429/MT3533.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                         126 LLGONTPAIAVNEAEYGEMWAQDAAAMFGYAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 GTAGKESVGQPAGL 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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006246;
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YY29 MYCTU
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GGPLLGALAAAVVPGVAGLAGVAGLAAL-PAVGAA--AGAPAALVGSVAPVSGGVVSPQA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE=88295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Fornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Deciphering the blology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-CDC 1551 / Oshkosh,
MEDINE-CDC 1551 / Oshkosh,
MEDINE-2206494; PubMed=12218036;
MEDINE-2206494; PubMed=12218036;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Bishai W., Jacobs W.R. T., Weidman J., Khouri H., Gill J., Mikula A.,
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                  324 WAAANQAVTPAARALPLISLISAAERGPGOMLGGLPVGOMGARAGGGLSGV 374
                                                                                       Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 184:5479-5490(2002).
--- SIMILARITY: Belongs to the mycobacterial PPE family.
--- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 82.
                                                                                                                                                                                                                                                           YU21_MYCTU STANDARD; PRT; 435 AA.
053268; 053269;
16-0CT-2001 (Rel. 40, Last sequence update)
11-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
12-0CT-2003 (Rel. 42, Last annotation update)
13-0CT-2003 (Rel. 42, Last annotation update)
14-0CT-2003 (Rel. 42, Last annotation update)
15-0CT-2003 (Rel. 42, Last annotation update)
16-0CT-2003 (Rel. 42, Last annotation update)
17-0CT-2003 (Rel. 42, Last annotation update)
18-0CT-2003 (Rel. 43, Last annotation update)
18-0CT-2003 (Rel. 40, Last annotation update)
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Tuberculist; Rv3022c; -
Tuberculist; Rv3022c; -
InterPro; IPR00030; Microbac_PPE.
InterPro; IPR00030; Microbac_PPE.
Hypothetical protein; Complete proteome.
CONFLICT 299 299 G -> A (IN REF. 2).
CONFLICT 317 320 LAGV -> VTGL (IN REF. 2).
SEQUENCE 326 L -> V (IN REF. 2).
SEQUENCE 435 AA; 42876 MW; 3B157643BAA8484A CRC64;
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EMBL; AL021287; CAA16107.1; ALT_FRAME.
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IIGR; MT3106; -.
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 -------WIN------WINDWEFATVGFALGVFVLVPLLEFAVVLE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 GGGVAANLGRAASV-GSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 MSMTNSGVSMTNTLSS------MLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGL 301
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                                                                                                                                8 ASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSVVVAAVGGCWGVWQGPSAEL
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                                                                                    6 ALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGL
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D.; Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann, DeBoy W. Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F.; Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-9829597; PubMed-9634230;
MEDLINE-98295987; PubMed-9634230;
Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Bary C.E. III. Tekaia F., Badcock K., Bacham D., Chillingworth T., Comnor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagals K., Krogh A., McLean J., Moule S., Murphy D., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Sustoon J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sustoon J., Whitchead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Indels 107;
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(1) TaxID=1773;
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-!- SIMILARITY: Belongs to the mycobacterial PPE family. Hypothetical protein, Complete proteome. SEQUENCE 178 AA; 19811 MW; 8BE1FC025ABFBEA6 CRC64; 184:5479-5490 (2002) TIGR, MT3533; Tuberculist, Rv3429; Interro; IRR000030; Microbac_PFE.
Pfam; PF00823; PPE; 1. ; AE007158; AAK47873.1; C70975; C70975. EMBL; Z95389; CAB08678.1; 65; Conservative strains. Query Match Best Local Similarity Matches a g ò

120 ILIATNILIGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEBAPEMTSAG 179 G 180 G 177 180 à 요 ð

01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv3425. Mycobacterium tuberculosis. RV3425 OR MTCY78.04C YY25 MYCTU Q50703;

MEDLINE=9829597; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris J. Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekaia F., Badcock K., Bacham D., Shown D., Chillingworth T., Comnor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Noule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998). Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium. NCBI_TaxID=1773, SEQUENCE FROM N.A.

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STRAIN=BALB/C; TISSUB=Lung;
MEDLINE=95130069; PubMed=7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin mouse chromosome 5 in a region of linkage conservation with 83; Indels SIMILARITY: Belongs to the mycobacterial PPE family. Hypothetical protein, Complete proteome. SEQUENCE 176 AA; 19855 MW; BRCEF2E9463B87B0 CRC64; 11.2%; Score 217.5; DB 1; 33.5%; Pred. No. 2.3e-06; iive 31; Mismatches B3; 01-0cT-1996 (Rel. 34, Created) 01-0cT-1996 (Rel. 34, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) Elastin precursor (Tropoelastin). 860 AA EMBL; Z77165; CAB01031.1; -.
PIR; F70738; F70738.
Tubercutist; Rv3425; -.
Interro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1. Genomics 23:125-131(1994). Conservative STANDARD; Mus musculus (Mouse) Local Similarity es 58; Conserv NCBI_TaxID=10090; MOUSE Query Match DATE THE TRANSPORT OF THE PARTY AND THE PART ò 셤 8 g

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genome sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.9%; Score 153.5; DB 1; Length 860;
24.4%; Pred. No. 0.068;
vative 34; Mismatches 192; Indels 131; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 AERGP---GOMLGG--LPVGQMGARAGGGLS------GVLRVPPRPY 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  785 ÁKYGAAGLGGVLGARPFÞGGGVAÁRÞGFGLSPIYPGGGAGGLGVGGKÞÞKÞY 836
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                              ELASTIN.
BY SIMILARITY.
', OCOBESAAEIEDD7F1 CRC64;
PIR; A55721; EAMS.
MGD; MGI:95317; Eln.
InterPro; IPR003979; tropoelastin.
PRINTS; PRO1500; TROPOELASTIN.
Structural protein; Repeat; Signal; Connective tissue.
SIGNAL 1 27 POTENTIAL.
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16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv3426.
RV3426 OR MTCY78.03C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 AA.
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MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                               71955 MW;
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                                                                                                                                                                                                                                                                 Matches 115; Conservative
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Q50702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 VAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 ADAALRYLDWISKHSRQILRTARVIESLVMAYEETLLRVVPPATIANNREEVRRIJASNV 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.
-i- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEGUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-S104868; Pubmed=1702999;
Pierce R.A., Deak S.B., Stolle G.A., Boyd C.D.,
"Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [3] SECUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92241859; PubMed=1572637;
Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
"Elements of the rat tropoelastin gene associated with alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.8%; Score 151.5; DB 1; Length 232; 35.2%; Pred. No. 0.021; ive 18; Mismatches 60; Indels 1;
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SEQUENCE OF 781-864 FROM N.A.
MEDLINE-88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
"Rat tropoclastin is synthesized from a 3.5-kilobase mRNA.";
"Rat tropoclastin is synthesized from a 3.5-kilobase mRNA.";
"Rat tropoclastin is synthesized from a 3.5-kilobase mRNA.";
Nature 393:537-544(1998).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1] protein; Complete proteome.
232 AA; 25872 MW; D76512D49EB272C6 CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; G70738; G70738.
Tuberculist; Rv3426; -
Interpro; IPR000030; Microbac_PPE.
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                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z77165; CAB01030.1; -.
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Matches 43; Conservative
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Hypothetical protein, C
SEQUENCE (232 AA: 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- IGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform 2, isoform 5, isoform 7 and isoform 8).

/FILE-OSP 0004244.
Missing (in isoform 3, isoform 5, isoform 6 and isoform 8).

/FILE-OSP 0004245.
Missing (in isoform 4, isoform 6, isoform 7, and isoform 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 GGIPGVGGPGIGGPGIVGGPGAVSPAAAAAAAKAAK--YGARGGVGIPTYGVGAGGFPG 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 150; DB 1; Length 864;
25.9%; Pred. No. 0.11;
tive 31; Mismatches 153; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                         IsoId=Q99372-8; Sequence=VSP 004244, VSP_004245, VSP_004246; PTM: The crosslinks are made of deaminated Lys.
SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers. ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=8;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIG=VSP 004246.
456894BB09E79FD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
Structural protein; Connective tissue; Repeat; Signal;
                                                                                                                                                                                                                                 Name=6;
IsoId=Q99372-6; Sequence=VSP_004245, VSP_004246;
                                                                                                                                                                                                                    IsoId=Q99372-5; Sequence=VSP_004244, VSP_004245;
                                                                                                                                                                                                                                                                              IsoId=Q99372-7; Sequence=VSP_004244, VSP_004246;
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                                                                                                                                                                                     IsoId=099372-4; Sequence=VSP_004246;
                                                                                                                           IsoId=Q99372-2; Sequence=VSP_004244;
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                                                                                      near;
IsoId=099372-1; Sequence=Displayed;
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EMBL; M66372; AAA42268.1;

EMBL; M86372; AAA42271.1;

EMBL; M86363; AAA42271.1; JOINED.

EMBL; M86363; AAA42271.1; JOINED.

EMBL; M86364; AAA42271.1; JOINED.

EMBL; M86371; AAA42271.1; JOINED.

EMBL; M86371; AAA42271.1; JOINED.

EMBL; M86373; AAA42272.1; JOINED.

EMBL; M86373; AAA42272.1; JOINED.

EMBL; M86375; AAA42272.1; JOINED.
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DISULFID
VARSPLIC
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	005298 mycobacteri Q7u0e9 mycobacteri	Q7u071 mycobacteri O8viz3 mycobacteri		Q7twf5 mycobacteri	Q7tzj3 mycobacteri	O53939 mycobacteri	Q99qil mycobacteri	O53957 mycobacteri	-	Q7tzh8 mycobacteri	O53956 mycobacteri	O53950 mycobacteri	Q7tzi4 mycobacteri	Q9z5k0 mycobacteri
SUMMARIES	005298 Q7U0E9	Q7U071 O8VIZ3	O06341	Q7TWFS	Q7TZJ3	053939	Q99Q11	053957	Q7TZH7	Q7TZH8	053956	053950	Q7TZI4	Q9Z5K0
DB	16	16	16	16	16	16	N	16	9	16	16	16	16	16
% Query Match Length DB	391	9 6 6 7 8 8 8 8 8 8	393	393	393	411	410	409	409	399	403	423	423	421
% Query Match	100.0	91.3	81.2	81.2	40.0	40.0	38.7	38.5	38.4	38.0	37.8	37.8	37.8	37.5
Score	1920.5	1779.5	1583	1583	779.5	779.5	754	751	749	740.5	737.5	736	736	731
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MEDLINE=22709107; PubMed=12788972;

MEDLINE=22709107; PubMed=12788972;

Ranner T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Parris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

"The complete genome sequence of Mycobacterium bovis.";

"The Acad. Sci. U.S.A. 100:7877-7882(2003).
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99.0%; Pred. No. 8.4e-101;
tive 2; Mismatches 1; Indels 1;
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                                                                                                                                 Length
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391 AA; 39158 MW; E409396B3ABDC0F8 CRC64;
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                                                                                                                             Score 1949; DB 16;
Pred. No. 2.1e-102;
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EMBL; 293777; CAB07839.1; -... EMBL; AE007000; AAK45491.1; -... EMBC.8; B70608. TIGR; M71234; -... TUGR; M71234; -... Tuberculist; Rv1196; -... Tuberculist; Rv1196; -... Thypothetical PRE; Hypothetical protein; Complete prote SEQUENCE 391 AA; 39158 MW; E4093
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Best Local Similarity 100.0%;
Matches 391; Conservative 0
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PPE18 OR MB1228.
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MEDINE=22702107;
Diblore FROM N.A.
MEDINE=22709107;
MEDINE=22709107;
Dubhoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkill J., Barrell B.G., Colle S.T., Gordon S.V., Hewinson R.G.;
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
BMEJ: BX248338; CAD94257.1;
COMPLETE PROCESSION, 698A92A50B33F CRC64;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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MEDLINE=98295987; PubMed=9634230;
GOLG S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Davies R., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamilin N., Holroyd (Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Sulter S., Seeger K., Whitehead S., Barrell B.G.; Sulares R., Sularing the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 393;
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome sequence.";
Nature 333:537-544(1998).
EMBL, 295390; CAB08702.1; -.
PIR, C70568;
Tuberculist; Rv3478; -.
InterPro; IPR00030; Microbac_PPE.
Pfam, PR00823; PEF. I.
Pfam, PR00823; PEF. I.
SEQUENCE 393 AA; 39413 MW; AF4C20C95DAE7DD4 CRC64;
                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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|GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
                                                                                                                           GLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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81.5%; Pred. No. 9.3e-82;
ive 20; Mismatches 47
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                                                                                                                                                                                                                                                                                       Created)
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01-JUL-1997 (TrEMBLrel. 04,
01-JUN-2003 (TrEMBLrel. 24,
Hypothetical protein Rv3478.
RV3478 OR MTCY13E12.31.
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Matches 322, Conservative
                                                                                                                                                                                                                                                  PRELIMINARY;
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STRAIN-CDC 1551 / Oshkosh;

Reischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVDFGALPPEINSARMYAGPGSASLVAAAKMWDSVASDLFSAASAFQSVVWGLTTGSWIG
                          LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHLSPISN
                                                                                                 241 IVSMLNNHVSMTNSGVSMTNTLHSMLKGFAP-AAAQAVETAAQNGVQAMSSLGSQLGSSL
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                                                                           MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL
                                                                                                                                              GSSGLGGGCVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG
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     LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
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84.8%; Pred. No. 2e-85;
ive 20; Mismatches 34; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AE0071L1, AAK47941.1; -.
TIGR; MT3582; -.
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GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000030; Microbac_PPE.
InterPro; IPR0000508; Peptidase_S26.
Pfam; PP00823; PPE; 1.
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Last sequence update)
Last annotation update)
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SEQUENCE 393 AA; 39688 MW; 86F0B67798855511
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01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
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                                                                                                                                                                                                                    GLPVGQMGARAG-
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Last sequence update) Last annotation update)

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   01-0CT-2003
01-0CT-2003
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300 GSSGLGAGVAANLGRAASVGSLSVPPAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy. S., Grondin S., Jacotoix C., Monsempe C., Simon S., Harris B., Akkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G., "The complete genome sequence of Mycobacterium bovis.", Proc. Natl. Acad. Sci. 012, 35.A. 100:7877-7882(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                               360 GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
                                                                                                        357 GLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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|GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
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STRAIN=AP2122/97;
MEDLINE=22709107; PubMed=12788972;
                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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PPE60 OR MB3505.
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SEQUENCE 393 AA
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O7TWF5;
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121 ISTINVEGONTSAIAAAEAQYGEMWAQDSAAMYAYAGSSASASA-VTPESTPPQIANPTAQ 179
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
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STRAIN-AF2122/97;
MEDLINE-22709107;
MEDLINE-22709107;
Darnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Monseyer C., Simon S.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monseyer C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
"The complete genome sequence of Mycobacterium bovis.";
"The Acad. Sci. U.S.A. 100:7877-7882(2003).
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Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PEF-family protein.
RV1789 OR MT1838 OR MTV049.11.
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40.0%; Score 779.5; DB 16;
Best Local Similarity 43.7%; Pred. No. 2e-36;
Matches 179; Conservative 65; Mismatches 129;
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291 SLGSSLGS----SGLGGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTS 345
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Mycobacterium microti.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1806;
                                                                                        SEQUENCE FROM N.A.

STRAIN=myc 94-2272, and 0V254;
Sivadon V., Heym B., Mazancourt P., Gaillard J.-L.L.;
Sivadon V., Heym B., Mazancourt P., Gaillard J.-L.L.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF335180; AAK20894.1; -.
EMBL; AF335199; AAK20893.1; -.
InterPro; IFR000030; Microbac_PPE.
Pfam; PP00823; PPE; I.
SEQUENCE 410 AA; 40044 MW; 3B9DA3174655A5EA CRC64;
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Best Local Similarity 44.5
Matches 177; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 SISALLTDIQPYASFFYNTEGLPYFSIGMGNNFIQSAKTL-GLIGSAAPAVA----AA
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                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17711.1; ALT_INIT.
BMBL; AL002043; AAK46108.1; -.
TIGR; G70929; G70929.
TIGR; MIS38; -.
TUBECULIST; RV1789; -
Tuberculist; RV1789; -
Tuberculist; RV1789; -
Tuberculist; PR000030; Microbac_PPE.
                                             Ω,
     Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Davlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oldver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Suston J., Whitehead S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.0%; Score 779.5; DB 16; Length 411; 43.7%; Pred. No. 2.1e-36; Live 65; Mismatches 129; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 AA; 40557 MW; 03C90B5E0590B7DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179; Conservative
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE 411 AA
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Gaps

30;

Length 410;

38.7%; Score 754; DB 2; Length 41 44.5%; Pred. No. 5.7e-35; Live 51; Mismatches 140; Indels

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SEQUENCE FROM N.A.
MEDLINE=96295997; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
Cole S.T., Brosch R., Parkhill J., Bary C.B. III. Tekaia F.,
Badcock K., Basham D., Ercom D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Ouail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
                                                      01-UN-1998 (TTEMBLrel. 06, Last sequence update)
01-UN-2003 (TTEMBLrel. 24, Last annotation update)
PPB-family protein.
8V1808 OR MT1856.1 OR MTV049.30.
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridee; Actinomycetales; Corymebacterines; Mycobacterium.
NCBI TaxII=1773;
409
                                       01-JUN-1998 (TrEMBLrel. 06, Created)
  PRELIMINARY;
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Created)
Last sequence update)
Last annotation update)

Q99Q11 PRELIMINARY; Q99Q11, O1-JUN-2001 (TEMBLEE] 17, Ca O1-JUN-2001 (TEMBLEE] 17, Le O1-OCT-2002 (TEMBLEE]. 22, Le RV1808-like protein.

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12:10:38 2004

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Wed Jul

DB 16; Length 399;

38.0%; Score 740.5;

Query Match

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180 AAQSAVVAQAAGAAASDITAQLSQLISILPSTIQSLA--TTATATSASAG--WDTV--- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VATNIFGONTPALAATEAHYAEMWAQDAAMYGYAGSSATA-SQLAPFSEPPOTINPSAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 LEQAAAVEEASDTAAA-----NQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 RSPISNMVSMANNHMSMTNSGVS-----MTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAM 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 LQSITTILANLTGPYSIIGLGAIPGGWWLTFGQILGLAQNAPGVAALLGPKAAAGALSPL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSL-GSSLGS-SGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSA- 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATATLLPFEEAPEMTSAGGL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                              STRAIN-CDC 1551 / Oshkosh,
STRAIN-CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey B.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 APĹRGGYIGDITPLGGGATGGIAKÁIYVGSLSVÞQGWÁBAAPVMRAVÁSVLÞGÍGAAPÁL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Gaps
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                       laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17729.1;
EMBL; AR007044; AAK46129.1; ALT_INIT.
PIR; A70932; A70932.
TIGR; WH1856.1;
Tuberculist; RV1808;
InterPro; IPR000030; Microbac_PPB.
Fam; PP00823; PPB; 1.
Complete proteome.
SEQUENCE 409 AA; 39917 MW; 1B15202BACF36379 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.5%; Score 751; DB 16; Length 4
Best Local Similarity 44.7%; Pred. No. 8.4e-35;
Matches 177; Conservative 53; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 AERGPGOMLGGLPVGOMGARAGGGL----SGVLRV 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : : : | | AAEAPGALFGEMALSSIAGRALAGTAVRSGAGAARV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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25,
25,
                                 complete genome sequence.";
Nature 393:537-544(1998).
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium bovis.
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PPE32 OR MB1837.
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 LQSITTILANLTGPYSIIGLGAIPGGWWLTFGQIL-GLAQNAPGVAALLGPKAAAGALSP 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 LEQAAAVEEASDTAAA-----NQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH
                                                                                                                                                                                                                                                                2 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 RSPISNMVSMANNHMSMTNSGV---SMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS
                                                                                                                                                                                                                                  Gaps
                                Garnier T., Biglmeier K., Camus J.-C., Medina N., Manscor H., Pyor M., Duthoy S., Grondin S., Lacroix C., Moneempe C., Simon S., Harris B., Atkin R., Dogett J., Mayes R., Keating L., Wheeler P.R. Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; Proc. Natl., Acad. Sci. U.S.A. 100:7877-7882 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22709107; PubMed=12788972; Medina N., Mansoor H., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor: M., Duthoy, S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis.", Proc. Natl. Acad. Sci. US.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                38.4%; Score 749; DB 16; Length 409; 44.3%; Pred. No. 1.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium bovis.
Bacteria, Actinobacteridae, Actinomycetales, Corymebacterinaee, Mycobacteriaceae, Mycobacterium.
NCBI TaxID=1765;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                               409 AA; 39931 MW; D57892628B131A9E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Mismatches 140;
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                 MEDLINE=22709107; PubMed=12788972;
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                                                                                                                                                                                                                                 Matches 176; Conservative
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PPE31 OR MB1836.
                                                                                                                                                                                                               Similarity
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                                                                                                                                                  Complete proteome.
SEQUENCE 409 AA;
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SEQUENCE 399 AA;
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                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                   Local
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EMBL/GenBank/DDBJ databases
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                                                                                                                      PIR; H70931; H70931.
TICR; MT4856; -.
Inbercutist; Rv1807; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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RV1801 OR MTV049.23 OR MT1850.
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laboratory strains.";
Submitted (AER-2001) to the
EMBL; ALO22021; CRA1728.1;
EMBL; AE007044; AAK46128.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       227
                                                                                                                                                                                                                                                                                                                                                         238 2
403 AA;
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                                                                                                                                                                                                                                                                                            Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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MEDILINE=9829897; PubMed=9634230;

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

B Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

B Badcock K., Basham D., Errown D., Chillingworth T., Cornor R.,

A Badcock K., Estylewell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                        62 SAGLMVAAASPYVAMMSVTAGGAELTAAQVRVAAAAYETAYGLTVPPPVIAENEAELMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 ---GLWKTVSPHRSPISNMVSMANNHMSMTNSGVSM-TNTLS---SMLKGFAPAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 WLDKLWALLDPN-----SNFWNTIASSGLFLPSNTIAPFLGLLGGVAAADAAGDV
                                                                                                                                    1 MDFATLPPEINSARMYSGAGSAPMLAAASAWHGLSAELRASALSYSSVLSTLTGEEWHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 LEQAAAVEEASDTAAA-----NOLMNNVPQALQQLAQPTQGTT---PSSKLG-----
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                                                                                                  VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                     60; Mismatches 122; Indels
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
      Pred. No. 3.2e-34;
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RV1807 OR MT1856 OR MTV049.29.
   42.8%;
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                                     Matches 182; Conservative
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   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 KLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSM-TNTLS---SMLKGFAPAAAAQAV 278
                                                                                                                                                                                                                                                                         294 LGEATSG-----GLGGALVAPLGSAGGLGGTVAAGLGNAATVGTLSVPPSWTAAAPLASP
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                                                                                                                                                                               Gaps
                                                                                                                                                                               61;
                                                                                                                      37.8%; Score 737.5; DB 16; Length 403;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                            ; Pred. No. 4.8e-34;
60; Mismatches 123; Indels
227 F -> S (IN REF: 2).
238 V -> L (IN REF. 2).
39243 MW; DCE18880FD15CBFE CRC64;
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Last annotation update)
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377 VPPRPYVMPHSPAAG 391
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              Mycobacterium bovis.
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                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                         Complete proteome. SEQUENCE 423 AA;
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                                                                                                            STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Hickey E.,
Fletson J., DeBoy R., Godson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                          62 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
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179 GAQSSAVAQTAATAAGGNLQSAFPQLLSAVPRALQGLALPTASQSASATPQMVTDLGNLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || || || || || || || || || || TÒNGQGVSALIGKIGGKPITGALAPIAEFALHTPILGSEGLGGGSVSAGIGRAGLVGKLS
                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and
Rutter S., Seeger K., Skelton S., Squares M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Ocomplete genome sequence.";

Nature 393:537-544(1998).
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                                                                                                                                                                                                     423 AA; 41477 MW; 26E52CC271FBBF57 CRC64;
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InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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SEQUENCE 423 AA
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                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Query Match
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Pryor M., Duthoy's., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
Bacteria; Actinomyceria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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37.8%; Score 736; DB 16; Length 4
Best Local Similarity 41.8%; Pred. No. 6.2e-34;
Matches 182; Conservative 50; Mismatches 123; Indels
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MEDLINE=22709107; PubMed=12788972;
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COMPANY Patent D 2025101494-A 1 09-APR-2002; COMPANY CORP. 1 09-APR-2002; COMPANY CORP. 1 09-APR-2002; PER	601 TTCAGTCGGTGGTCTGACGGTGGGGTCGTGATAGGTTCGTCGGCGGGGTCTGA 660 601 TTCAGTCGGTGGTCTGACGGTGGGGTCGTGATAGGTTCGTCGGCGGGGTCTGA 660 601 TTCAGTCGGTGGTCTGGGTCGGGTGGGTCGTGGTTGGTCGGCGG	1021 CCGCGGTCGAGGGCTCCGACACCGCGGGGAACCAGTTGATGAACAATGTGCCCC 1080 1021 CCGCGGTCGAGGGCTCCGACACCGCGGGGGGACCAGTTGATGAACAATGTGCCCC 1080 1021 CCGCGGTCGAGGCCTCCGACACCGCGGGGGGCCCCGGTTGATGAACAATGTGCCCC 1080 1081 AGGCGCTGACACACGCCCAGCCCAGCACCAGCACCCTTCTTCCAAGTTGGTG 1140 1141	ACAACCACATGTCGATGACCAACTCGGGTGTGTCGATGACCAACACCTTGAGCTCGATGT	1411 CGGCCAACCAGCAGCGGGGGGGGGGGGGGGGGGGGGG
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YASIR A W SKEIKY, MARK ALDERSON, ANTONIO CAMPCS NETO PC
C12N15/09, A61K39/04, A61K48/00, A61P31/04, C07K14/35, C07K19/00, PC
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CC Description of Artificial Sequence: bi-fusion
protein TbH9-Ra35
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FH Key Location/Qualifiers FT CDS (1)(1791). FEATURES Location/Qualifiers 11797 /organism="synthetic construct"	/mol type="genomic DNA" /db_xref="taxon:32630" Query Match	tches 1772; Conservative 0; Mismatches 2; Indels 0; Gaps 464 CATGGTGGATTTCGGGGCGTTACCACCGGAGATCAACTCCGCGAGAACATGTACGCCGGCCC 24 CATGGTGATTTCGGGGCGTTACCACCAGAACAACAACAACAACAACAACAACAACAACAA	524 CATUCACCCTCGCTGGTGGCCCGGCCTCGAAATCAACCGGAGGATGACGCGGGCGAGTGACCTGGCCGAGTGACCTGGCGAGTGACCTGGCGAGTGACCTGGCGAGTGACCTGGCGAGTGACCTGGCGAGTGACCTGGCGAGTGACCTGGCGAGTGACCTGGCGAGTGACCTGGCGAGTGACCTGAGAAACGTGGGAAACGATGACTGAGAAACGATGAACTGAAAACGATGAACTGAAAACGATGAAAACGATGAAAACGATGAAAACGATGAAAACAGAAAAAAAA	TCGGCGTTTCAGTCGGTGGTCTGAGGTCTGACGGTGGGGTCGTGGATAGG 64	Qy 644 TICGICGCGGGTCTGANGGTGGCGGCGGCCTCGCCGTATGTGGCGTGANGACGTCAC 703 Db 204 TICGICGCGGGTCTGANGGTGGCGGCGCTCTGGCGGTATGTGGCGTGATGAGGGTCAC 263	Qy 704 CGCGGGGCAGGCCGAGGCTGCCCCCAGGTTGCTGCGGGGCCTACGAGAC 763 Db 264 CGCGGGGCAGGCCGAGGTGCCCCAGGTTCCTGCGGCCTACGAGC 323	OY 764 GGCGTATGGGCTGACGGTGCCCCGCCGGTGATCGCCGAGAACCGTGCTGAACTGATGAT 823 Db 324 GGCGTATGGGCTGACGGTGCCCCGCCGGTGATCGCCGAGAACCGTGCTGAACTGATGAT 383	OY 824 TCTGATAGCGACCTCTTGGGGCAAAACACCCCGGCGATCGCGGTCAACGAGGCCGA 883 Db 384 TCTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGGGATCGCGGTCAACGAGGCCGA 443	QY 884 ATACGGCGAGATGTGGGCCCAAGACGCCGCGGGATGTTTGGCTACGCCGCGGGGCGACGACGCGCGGCGAGGCGAGATGGCTACGCCGCGGGGCGACGCGGCGAGGTGGGGCGAGGCGAGGCGAGGTGGGGCGAGGAG	QY 944 GACGGCGACGTTGCTGCCGTTCGAGGAGGCCCGGAGATGACCAGCGCGGGTGG 1003 Db 504 GACGGCGACGACGTTGCTGCCGTTCGAGGAGGCCCGGAAATGACCAGCGCGGGGGGG 563	Qy 1004 GCTCCTCGAGCAGGCCGCGGTCGAGGAGGCCTCCGACACACCGCGGAAACCAGTT 1063 Db 564 GCTCCTCGAGCAGGCCGCCGCGGGGACCCTCCGACACCGCGGGGGAACCAGTT 623	Qy 1064 GATGAACAATGTGCCCCAGGCGCTGCAACCCCAGGCCCACGCCAGGCACCCAGGCC 1123 Db 624 GATGAACAATGTGCCCCAGGCGCTGCAACCCAGCCCAGGCCACGCAGGCCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCAGGCCAGGCCCCAGGCCCAGGCCAGGCCCCAGGCCCAGGCCCAGGCCAGGCCCCAGGCCCAGGCCAGGCCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCAGGCCAGGCCCCAGGCCAGGCCAGGCCCCAGGCCCAGGCCCCAGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCCAGGCCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCAGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGCCCCAGGCCCCAGCCCCAGCCCCAGCCCAGGCCAGCCCCAGCCCAGCCAGCCAGCCAGCCAGCCAGCCCAGCCCCAGCCCAGCCCCAGCCCAGCCCAGCCCCAGCCCAGCCCAGCCAGCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCAGCCCCAGCCCCAGCCCCCAGCCCCCAGCCCCCAGCCCCCC	QY 1124 TTCTTCCAAGCTGGGTGGCTGTGGAAGACGGTCTCGCCGCATCGGCGGTCGCGAA 1183 Db 684 TTCTTCCAAGCTGGCTGTGGAAGACGGTCTCGCCGCATCGGTCGCCGATCAGCAA 743	Oy 1184 CATGGTGTCGATGGCCAACACACATGTCGATGACCAACTCGGGTGTGTCGATGACCAA 1243 Db 744 CATGGTGTCGATGGCCAACAACATGTCGATGACCAACTCGGGTGTGTCGATGACCAA 803	QY 1244 CACCTTGAGCTCGATGTTGAAGGCTTTGCTCCGGCGGCCCCCCCC	QY 1304 CGCGGCGCAAAACGGGGTCCCGGCGATGAGCTCGCTGGGCACTCGCTGGGTTCTTCGGG 1363 Db 864 CGCGGCGCAAAACGGGGTCCGGGGGTTCGGTGGGTCGCTGGCTCGCTGGGTTCTTC	

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TITLE Fusion proteins of Mycobacterium tuberculosis antigens and their uses JOURNAL Patent: US 6627198-A 25 30-SEP-2003; FEATURES 1. 1797 Source /organism="unknown" ORIGIN Query Match Best Local Similarity 99.9%; Pred. No. 1.7e-209; Matches 1772; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	464 CATGGTGGATTTCGGGGCGTTACCACCGGAGATCAACTCCGCGAGGATGTACGCC 24 CATGGTGGATTTCGGGGCGTTACCACCGGAGATCAACTCCGCGAGGATGTACGGCC 524 GGGTTCGGCCTGGTGGCCGCGGCCTCAGATGTGGGACGAGGGTGACGCCGGGTGACGAGGTGACGCCGGCTCAGATGTGGGACGTGACGCGGGGGAGTGACGAGGGGGGGG	144 Trogecegered for the first of the fi	DB 284 CGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	OY 884 ATACGGCGAGATGTGGGCCCCAAGACGCCGCGGATGTTTGGCTACGCCGCGGCGACGGC 943 444 ATACGGCGAGATGTGGGCCCCAAGACGCCGCGCGATGTTTGGCTACGCCGCGGCGACGGC 503 OY 944 GACGGCGACGACGACGTTGCTGCCGTTCGAGGAGGCGCGGAAGATGACCAGCGCGGGGGGGG		OY 1184 CATGGTGTCGATGGCCAACAACCACTGGATGTCGATGTCTGGTGTGTCCCAA 1243 Db 744 CATGGTGTCGATGGCCAACAACCACATGTCGATGACCAACTCGGGTGTGTCGATGACCAA 803 OY 1244 CATGGTGTCGATGTTGAAGGGCTTTGCTCCGGGGGGGGGG

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Reed,S.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A.
Fusion proteins of Mycobacterium tuberculosis antigens and their
                                            624 GATGAACAATGTGCCCCAGGCGCTGCAACAGCTGGCCCAGCCCACGCAGGGCACCACGCC 683
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="teaxon:32630"
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GITCGTCGGCGGGTCTGATGGTGGCGGCGGCCTCGCCGTATGTGGCGTGGATGAGCGTCA
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S Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S. and Twardzik, D.R., Compounds and methods for immunotherapy and diagnosis of tuberculosis
AL Patent: US 6290969-A 106 18-SEP-2001;
Location/Qualifiers
II. 3058
/organism="unknown"
/mol_type="unassigned DNA"
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                          ACACCTTGAGCTCGATGTTGAAGGGCTTTGCTCCGGCGGCGGCCGCCAGGCCGTGCAAA
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Db 1171 ACACCTTCAGCTCCAATGCTCCGGCGCGCCCCAGCCCGTCGTTTTTTTT	Qy 1483 TGACCAGCCGCGGGAAAGAGGGCCCGGGCAGTGCTGCGG 1542 Db 1411 TGACCAGCTGACCAGCGCGGGAAGATGTGGGGGGGGGGG	RESULT 12	Reed, S.G., Skeiky, Y.A.W. and Dillon, D.C. Compositions and methods for the prevention and treatment of M. tuberculosis infection Patent: US 6350456-A lo6 26-FEB-2002; Location/Qualifiers 1. 3058 /organism="unknown" /mol_type="unassigned DNA" tch 51.1%; Score 1169; DB 6; Length 3058; al Similarity 99.6%; Pred. No. 2.7e-135;	Matches 1172; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Qy 463 TCATGGTGGATTTCGGGGGGTTACCACGGAGATCACTCCGCGAGGATGTACGCGGGC 522 Db 391 TAATGGTGGATTTCGGGGGGTTACCACGGGAGATCTACGCGGGCGC 450 Qy 523 CGGGTTCGGCCTCGCTGGTGGCGGCTCAGATGTGGGACGAGGATGTACGCGGC 450 Db 451 CGGGTTCGGCCTGGTGGGGGCTCAGATGTGGGACGGTGGCGAGTGACCTGT 582 Qy 583 TTTCGTGCTCGCTGGTGGCGGCTCTGGTTGTGGACGGTGGGGTGGCTGT 510	Db 511 TTTGGGCGCGTCGGCGTTGGTGGTGGTGGTGGGGTCTGACGGTGGGTG
XEYWORDS KEYWORDS SOURCE UNKnown. ORGANISM Unknown. ORGANISM Unknown. Lases it colors it colors. AUTHORS Reed.S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., vedvick, T.S. and Twandzik, D.R. TITLE JOURNAL Patent: US 633885.2-A 101 15-JAN-2002; FATURES SOURCE AUTHORS Reed.S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., vedvick, T.S. and methods for diagnosis of tuberculosis Location/Qualifiers 1. 3058 AUTHORS AUTHO	Query Match 51.1%; Score 1169; DB 6; Length 3058; Best Local Similarity 99.6%; Pred. No. 2.7e-135; Indels 0; Gaps 0; Matches 1172; Conservative 0; Mismatches 5; Indels 0; Gaps 0; QY 463 TCATGGTGGATTTCGGGGGTTACCACGGAGATCAACTCCGCGAGGATGTACGCGGGC 522 Db 391 TAATGGTGGATTTCGGGGGTTACCACGGAGATCAACTCCGCGAGGATGTACGCCGGCC 450 QY 523 CGGGTTCGGCGTTGGTGGCGGGGTTACCAGATGTGGGACAGCGTGGCGAGTGACCTGT 582 Db 451 CGGGTTCGGCTGGTGGTGGCCGGGGCTCAGATGTGGGACAGCGTGGAGTGACCTGT 510	Qy 583 TTTCGGCCGCGTCGGCGTTTCAGTCGGTGCTTGAGGGTCGTGGGTCGTGGGTCGGGTCGTGGATAG 642 Db 511 TTTCGGCCGCGTCGGCGTTTCAGTCGGTGCTCTGACGGTCGGGGTCGTGGATAG 570 Qy 643 GTTCGTCGGCGGTCTGATGGTGGGGGCGCTCGGCTGGTATGTGGGTGG	Oy 763 CGGCGTATCGGCTGACCCCCGGCGGTGATCGCCGAGAACCGTGCTGAACTGATGA 822 bb 691 CGGCGTATGGGCTGACGGTGCCCCGGCGGTGATCGCCGAGAACCGTGCTGAACTGATGA 750 Qy 823 TTCTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGCGATCGCGGTCAACGAGGCG 882 Db 751 TTCTGATAGCGACCAACCTCTTGGGGCAAACACCCCGGCGATCGCGGTCAACGGGGGGGG	Qy 943 CGACGGCGACGGCGACGTTGCCGCGAGGAGGCGCGGAGATGACCAGCGCGGGGTG 1002 Db 871 CGACGGCGACGGTTGCTGCCGTTCGAGGAGGCGCGCGAGATGACCAGCGCGGGGTG 930 Qy 1003 GGCTCCTCGAGCAGGCGGCGGGGGGGGGGGGGGGGGGGG	1123 CTTCTTCCAACTGGGGCCTGTGGAACAGCTCGCCGCATCGGTCGCCCGATCGGCCGATCGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGCGATCGCCGATCGCCGATCGCCGATCGCCGATCGCCGATCGCCGATCGCCGATCGCCGATCGCCGATCGCCGATCGCCGATCGAT

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763 CGGCGTATGGGCTGACGGTGCCCCGCCGGTGATGACGCGAGAACCGTGCAGTGATGA 822 	823 TTCTGATAGCGACCTCTTGGGGCAAAACACCCCGGCGATCGCGGTCAACGAGGCCG 882 		943 CGACGGCGACGTGCTGCTGCCGTTCGAGGAGGCGCCGGAGATGACCAGCGCGGGTG 1002 	1003 GGCTCCTCGAGCAGGCGGCGGTCGAGGAGCCTCCGACACGCGGGGGGAACCAGT 1062 	1063 TGATGAACAATGTGCCCCGAGGCGCTGCAACAGCTGGCCCAGGCCCAGGGCACCAGGC 1122 	1123 CTTCTTCCAAGCTGGGTGCCTGTGGAAGACGGTCTCGCCGCATCGGTCGCCGATCAGCA 1182 	1183 ACATGGTGTCGATGGCCAACACACATGTCGATGACCAACTCGGGTGTGTCGATGACCA 1242 	1243 ACACCTTGAGCTCGATGTTGAAGGCTTTGCTCCGGCGGCCGGC	1303 CCGCGGCGCAAAACGGGGTCCGGGCGATGAGCTCGCTGGGCAGCTCGGGGGTTCTTCGG 1362 	1363 GTCTGGGCGGTGGCGCGAACTTGGGTGGGGCGCCTCGGTCGG	1423 TGCCGCAGGCCTGGGCCGGCCAACCAGCAGTCACCCCGGCGGCGCGCGC	1483 TGACCAGCCTGACCAGCGCGGGAAAGAGGCCCGGGCAGATGCTGGGCGGGTGCCGG 1542 	1543 TGGGGCAGATGGGGCCCAGGCCGGTGGGCTCAGTGGTGCTGCGTGTTCCGCCGC 1602 	1603 GACCCTATGTGATGCCGCATTCTCCGGCAGCGA 1639 	
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Location/Qualifiers
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA" . 0 Length 3058; Duery Match 51.1%; Score 1169; DB 6; Length 3 est Local Similarity 99.6%; Pred. No. 2.7e-135; Atches 1172; Conservative 0; Mismatches 5; Indels 1243 1303 1063 1123 511 631 883 1003 931 991 463 523 451 583 643 703 763 691 943 GIN <u>ک</u> ۾ ð 음 상 음

Unclassified.
1 (bases 1 to 3058)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,

PAT 20-DEC-2002

DNA

3058 bp DN Sequence 101 from patent US 6458366. AR233150 GI:27275586

RESULT 13
AR233150
LOCCUS
DEFINITION
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VERSION
VERSION
SOURCE
ORGANISM

Unknown. Unknown.

REFERENCE AUTHORS

	OY 883 AATAGGGGAGATGTGGGCCCAAGACGCCGCGCGATGTTTGGCTACGCGGGGGACGG 942	OY 943 CGACGGGGGGGGGGGTTGCTGCCGTTCGAGGAGGCGCGGAGATGACCAGCGCGGGTG 1002	OY 1003 GGCTCCTCGAGCCGCCGCGGTCGAGGCCTCCGACACGCCGCGGCGAACCAGT 1062	053 TGATGAACAATGTGCCCCAGGCGCTGCAACAGCTGGCCCAGGCCACGCAGGCACCAGGC 1122	OY 1123 CTICTICCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCGCATCGGTCGCCGATCAGCA 1182	OY 1183 ACATGGTGTGGAACGAACAACACATGTCGATGACCAACTGGGGTGTGTGGATGACA 1242	OY 1243 ACACCTIGAGCTCGATGTTGAAGGCTTTGCTCCGGCGGCCGCCGCCGGCCG	Oy 1303 CCGCGCGCAAAACGGGTCCGGGCGATGAGCTCGCTGGCACTCGCTCG	Qy 1363 GTCTGGGCGGTGGGCCCCCCAACTTGGGTCGGGCGCCTCGGTCGG	Oy 1423 TGCGGAGGCCTGGGCCCAACCAGGAATCACCCGGGGGGGG	OY 1483 TGACCAGCTGACCAGGGGAAAAGAGGGCCCGGGCAGATGCTGGGGGGGCTGCCGG 1542		Qy 1603 GACCCTATGTGATGCGGCATTCTCCGGCGGGA 1639	3058 bp	Sequence 100 IIOM Fatern AX429698 AX429698.1 GI:21540898		AUTHORS Reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L., Vedvick, T.S. and Twardalk, D.R. TITLE Compounds and methods for immunotherapy and diagnosis of tuberculosis	JOURNAL Patent: EP 1203817-A 106 08-MAY-2002; CORIXA CORPORATION (US) PEATURES Location/Qualifiers
Qy 1363 GTCTGGCGGTGGCCGCCAACTTGGGTCGGCGCGCCTCGGTCGG	Db 1291 GTCTGGGCGGTGGCCGCCAACTTGGGTCGGGCGCCTCGGTCGG	Db 1351 TGCCGAGGCCTGCGCCAACCAGCATCACCCCGGCGCGCGC	Db 1411 TGACCAGCCTGACCGCGGGAAAGAGGGCCCGGGCAGATGCTGGGGCGGCTGCCGG 1470 Qy 1543 TGGGGCAGATGGGCCGGTGGTGGTGGTGTGCTGCTGCTGCTGCTGTGTTCGCCGC	Db 1471 TGGGGCAGATGGCCCAGGGCCGGTGGTCTCTTTTTTTTTT	Db 1531 GACCCTATGTGATGCCGCATTCTCCGGCGGCTA 1567	AR353355 AR353355 3058 bp DNA linear PAT 17-AUG-2003 DEFINITION Sequence 106 from patent US 6592877.		ORGANISM Unknown. REFERENCE I (bases 1 to 3058) AUTHORS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,	ч	FEATURES Location/Qualifiers Source 13058 /organism="unknown" /mol_type="genomic DNA"	Y Match 51.1%; Score 1169; DB 6; Length 3058; Local Similarity 99.6%; Pred; No. 2.7e-135; Table 2.	TITCGGGGCGTTACCACCGGAGATCAACTCCGCGAGGATGTACGCCGCC 52		Qy 583 TITCGGCCGCGTCGCGTTTCAGTCGGTGTCTGGGGTCTGACGGTGGGGTGG 642	Oy 643 GTTCGTCGGCGGGTCTGATGGTGGCGGCCGCCTCGCCGTANGTGGCGTGATGAGGGTCA 702 Db 571 GTTCGTCGGCGGGTCTGATGGTGGCGGCGGCCTCGCCGTANGTGGCGTGGATGATGGTCA 630	Qy 703 CCGCGGGGCAGCCGAGCTGACCGCCCCCAGGTCCGGGTTGCTGCGGGGGGCCTACGAGA 762 Db 631 CCGCGGGGGAGGCGAGCTGACCGCCCCAGGTTGCTGCGGGGGCCTACGAGA 690	Qy 763 CGGCGTATGGGCTGACGGTGGTCCCCGGCGGTGATCGCCGGCACACCGTGCTGAACTGATGA 822 Db 691 CGGCGTATGGGCTGACGGTGCCCCGCCGGTGATCGACGGAAACCGTGCTGAACTGATGA 750	TICTGATAGCGACCAACCTCTTGGGGAAAACACCCGGGGATCGCGGTCAACGAGGCCG

Oy 1423 TGCCGCAGGCCT	Db 1411 TGACCAGCTGA Oy 1543 TGGGGCAGNTGG Db 1471 TGGGGCAGNTGG	1603 1531	Search completed: July 3, Job time : 8840 secs														
13058 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"	<pre>Query Match</pre>	391 TAATGGTGGATTTCGGGGCGTTACCACCGGAACTACCGCGAGGATGTACGCCGGCC 450 523 CGGGTTCGGCCTCGCTGGTGGCCGGGGCTCAGATGTGGGACAGCGGGGGGGG	583 TITCGGCCGCGTCGGCGTTTCAGTCGGTGGTCTCACGGTCTCACGGTGGGGTCGTGGATAG 642	643 GTTCGTCGGGGGGTCTCATGGTGGCGGCGCCTCGCCGTATGTGGCGGTCGATGAGCGTCA 702 	703 CCGCGGGGCCGAGGCGAGCCGCCCCAGGTCCGGGTTGCTGCGGCGGCCTACGAGA 762 	763 CGCGTATGGGCTGACGGTGCCCCGCGGTGATCGCCGAGAACCGTGCTGAACTGATGA 822 	823 TICTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGGGATGGCGGTCAACGAGGCCG 882 	883 AATACGGGGAGATGTGGGCCCAAGACGCGGCGGATGTTTGGCTACGCGGGGGACGG 942 	943 CGACGGCGACGTCGCTCGCCGTTCGAGGAGGCGCCGGAGATGACCAGCGGGGGTG 1002 	1003 GGCTCCTCGAGCAGGCCGCCGCGGTCGAGGCCTCCGACACCGCCGGGGGGAACCAGT 1062 	1063 TGATGAACAATGTGCCCCAGGCGCTGCAACAGCTGGCCCAGCCCAGGAGGGCACCACGC 1122 	1123 CTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCGCATCGGTCGCCGATCAGCA 1182 	1183 ACATGGTGTCGATGGCCAACCACATGTCGATGACCAACTCGGGTGTGTCGATGACCA 1242 	1243 ACACCTTGAGCTCGATGTTGAAGGCTTTGCTCCGGCGGGGCGGCCGCCAGGCCGTGCAAA 1302 	1303 CCGCGCCAAAACGGGGTCCGGGGGATGAGCTCGCTGGGCTCGCTGGGTTCTTCGG 1362 	1363 GTCTGGGCGGTGGCGCCAACTTGGGTCGGGCGCTCGGTCGG	

TOCOGCAGGCCTGGGCCACCAGGCAGTCACCCCGGCGGCGCGGGGCGCTGCCGC 1482 TGACCAGCCTGACCAGCGCCGCGCAAAGAGGCCCCGGGCAGATGCTGGGCGGGGCTGCCGG 1542 GGGGCAGATGGGCCCAGGCCGGTGGCTCAGTGGTGTGCTGCTGTTCCGCCGC 1602 ARCCTATGTGATGCCGCATTCTCCGGCAGCCGGCGA 1639

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New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium Vaccine, immunity, diagnostic agent, gene thexapy, TbH9, antigen, Ra35; Ra12, WTB72F, chimeric, gene, ds. Mycobacterium sp. MTB72F fusion protein encoding DNA. Location/Qualifiers 42. .2231 /*tag= a /product= "MTB72F fusion protein" Disclosure; Page 87-90; 155pp; English. Guderian J; AAD47083 standard; DNA; 2287 BP. 13-MAR-2002; 2002WO-US008223 13-MAR-2001; 2001US-0275837P. Mycobacterium sp. Mycobacterium tuberculosis. Chimeric. (revised)
(first entry) Skeiky Y, Brannon M, WPI; 2002-759844/82. P-PSDB; AAE29708. (CORI-) CORIXA CORP. WO200272792-A2 19-SEP-2002

The invention relates to a recombinant nucleic acid molecule encoding a

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fusion polypeptide. The polymucleotide sequence Mycobacterium sp. and a polypeptide or its fragm from TSA, LeIF, M15, and are used in methods for useful as vaccines to el microorganisms such as Loplypeptides are used for in vivo diagnostic agentin vivo diagnostic agentin vivo diagnostic agentin Nivo diagnostic agentin Nivo diagnostic agentin Nivo diagnostic agentin Nivo diagnostic agentin Nivo diagnostic agentin Nivo diagnostic agentin Nivo diagnostic agentin Nivo diagnostic agentin Mycobacterium sp. (Updatu Query Match Best Local Similarity 10 Matches 2287; Conservati 61 ACACGGCCGCGTCC 1 TCTAGAAATAATT 121 TCGGGCAGGCGATC 121 TCGGCCAGGCGAT 181 ATATCGGGCCTACO 181 ATATCGGGCCTACC GAGTCCAACGCGTC TGATCACCGCGGTC TGATCACCGCGGTC 1111111111111 TGACCGCCGCCCAG TGACCGCCGCCCAG 1 TCTAGAAATAATT 61 ACACGGCCGCGTC GAGTCCAACGCGT 361 ACGGCCATCATCC 361 ACGGGCATCATCC GTACAGGGAACGTC CGTTACCACCGGAC TGGCCGCGGCTCAC TTCAGTCGGTGGTC GTACAGGGAACGT CGTTACCACCGGA TGGCCGCGGCTCA TTCAGTCGGTGGT TGGTGGCGGCGGC Sequence 2287 BP; 372 241 241 301 301 421 421 481 481 541 541 601 661 601 661 721 \$ 성: 염. g ò g ò g ò CC q g ò δ à 8 ò q à

the recombinant nucleic acid comprises a heterologous not encoding an antigen or an antigenic fragment from a Leishmania polymucleotide sequence encoding a samment the Leishmania nolymucleotide.	OY 781 TGCCCCGCCGGTG 	GCCCCGCCGCTGATCGCCGAGAACCGTGCTGAACTGATGATTCTGATAGCGACCAACC 840
oolynuclectides. Sequences of ting immune response in mammer protective immunity against parainst in an and an and an and an an an an an an an an an an an an an	Oy 841 TCTTGGGGCAAAAC 	CTTGGGGGAAAACACCCCGGGGATCGCGGTCAACGAGGCCGAATACGGCGAGATGTGGG 900
if for enhancing the expression of polynuclectides, as sents and for raising antibodies in a non-human is used in gene therapy. The present sequence is a nictual mile fluid manner in a non-mile fluid man inches in a non-human is a sequence of the new fluid mile fluid manner in the fluid manner is a sequence of the new fluid mile fluid manner is a sequence of the new fluid	0y 901 CCCAAGACGCCCCC 	CCCAAGACGCCGCCGCGATGTTTGGCTACGCCGCGGCGACGGCGACGGCGACGGCGACGT 960
s and andarc	0y 961 IGCTGCCGTTCGAG(Db 961 IGCTGCCGTTCGAG(TGCTGCCGTTCGAGGGGCGCCGGAGATGACCAGGGGGGTGGGGCTCCTCGAGCAGCCG 1020
71, () sign 501 i; 0 0; 3 Cunst; 3%; Score 2284; DB 6; Length 2287; 0%; Pred. NO. 0; 0, Winnstahn	Oy 1021 CCGCGTCGAGGAG 	CCGCGGTCGAGGAGGCCTCCGACACCGCGGGGGAACCAGTTGATGAACAATGTGCCCC 1080
O, MISHMACHINES O, MICHIAAGANGANATATACATATGCATCACCATC 60	Oy 1081 AGGCCTGCAACAGC Db 1081 AGGCGCTGCAACAGC	AGGIGCTGCAACAGTGGCCCAGGCCAGGGCACCAGGCCTTCTTCCAAGCTGGGTG 1140
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GGGCCTTCCTCGGCTTGGGTTGTGTGTGTGTGTGTGTGT	0y 1261 TGAAGGGCTTTGCTC Db 1261 TGAAGGGCTTTGCTC	TGAÀGGCTTTGCTCCGGCGGCGCCCCCCAGGCCGTGCAAACGGGGGCGCAAAACGGGG 1320
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73CGGGG	Oy 1501 CCGGGGAAAGAGGGG 	CCGCGGAAAGAGGGCCCGGGCAATGCTGGCGGGCTGCCGGTGGGGGAAGATGGGCCCCA 1560
TCGCTGG	0y 1561 GGCCGGTGGTGGGG 	GGGCGGTGGTGGTCGGTGTGCTGCGTGTTCCGCCGCGACCCTATGTGATGCCGC 1620
TCGCCGT	Oy 1621 ATTCTCCGCAGCCC	ATTCTCCGCAGCCGCCGTATATCGCCCCGCCCGCCTTGTCGCAGGACCGGTTCGCCGACT 1680
rceccer Gercrea	Oy 1681 TCCCGGGGTGCCCC	CCCGGGGGTGGCCCCTCGACCGGTCGGCTCGCCCAAGTGGGGGCCACAGGTGGTCA 1740
GCCGAGC 72	Oy 1741 ACATCAACACCAACO Db 1741 ACATCAACACCAAAC	CATCAACACCAAACTGGGCTACAACAACGCCGTGGGCGCGGGACCGGCATCGTCATCG 1800
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AGGICCGGGITGCTGCGGCCGGCCTACGAGACGGCGTATGGGCTGACGG 780		C 19

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with the tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and constructed in a particular and munum response in a mammal, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the population of Mycobacterium infection. The fusion proteins and the Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as community and for raising anti-M. tuberculosis antibodies in a non-human partie of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents to intradermal skin test. The present sequence is a DNA encoding to the intradermal skin test. The present sequence is a DNA encoding to the month of the invention are useful as in vivo diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGTCCAACGCGTGGTCGGGAGCGCTCCCGGCGAAGTCTCCGGCATCTCCACCGGCGACG 300
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                                                                                Composition comprising MTB39 antigen and MTB32A antigen from
Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCTAGAAATAATTTTGTTTACTTTAAGAANGANATATACATTATGCATCACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ACACGGCCGCCCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.9%; Score 2284; DB 6; Length 2287; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2287 BP; 372 A; 717 C; 814 G; 381 T; 0 U; 3 Other;
                                                                                                                                                Claim 62; Page 103-106; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 2287; Conservative
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    CGTTCAGCGTCCGCTCCCGGCCAAACCTACGGCGTCGATGTGGTCGGGTTATGACCGCACCC 1920
                                                                                                1981 GCGGCGTCGCGGTTGGTGAGCCCGTCGTCGCGATGGGCAACAGCGGTGGGGCAGGGCGGAA 2040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB72F; Ral2-TbH9-Ra35; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium species MTB72F fusion protein encoding DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium sp.
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AAD28342
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Db 1621 ATTCTCGGCGCTGCCCTCGACCGGCCGGCCTTGTCGCAGGACCGGTTGCCGACT 1680 Qy 1681 TCCCGGCGCTGCCCTCGACCGGCGGCGCCCTGTTGGCAGGACCGGTTGCCGACT 1740 Db 1681 TCCCGGCGCTGCCCTCGACCGGTGGCTGCCCAAGTGGGCCACAGGTGTCA 1740 Oy 1741 ACATCAACAACTGGCTGCCGTGGCGCGTGGCGCCGCGGCCACGGTGTT 1740 Db 1741 ACATCAACAACTGGCTGCCTGGCGTGGCGCGCGGCCCGGCATCGTCATCG 1800 Db 1741 ACATCAACAACTGGCTGCTGACCGTGGCGGGGGCCGGGATCGTCATCG 1800 DC 1761 ACATCAACACAACTGGCTGACCAACACACACGGGGGGCCCGGCACCGACTCATCA 1800 DC 1761 ACATCAACGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	Qy 1861 CGTTCAGCGTCCGGCCAAACCTACGGCGTCGATGTGGTCGGGTATGACCGCACC 1920 Db 1921 AGGATGCGGTTCGGCCTGCGGTCGGTTGGTTCGGGTATGACCGCACC 1920 Qy 1921 AGGATGTCGGGTTGCTGCGGTGCCTGCTGCTGCTGCGGGTATGACCGCACC 1980 Db 1921 AGGATGTCGGGTTGCTGCGGTGCCTGCGTGCCTGCGTGCG	OP 2221 CCGCTCCTAGGATATCCATCACCTCGCCGCTCCAGCAGATCCGATTCAAAAG 2280 Db 2221 CCGCGTCCTAGGATATCCATCACTGGCGGCGCTCGAGCAGATCCGGNTGTAACAAAG 2280 OY 2281 CCCGAAA 2287 BESULT 3 AA220194 XX AC AA220194 XX Tobecoules, therapy, vaccine; numunogen; ss. Mycobacterium tuberculosis antigen fusion protein Mtb32A DNA. KW Therapy; vaccine; numunogen; ss. Mycobacterium tuberculosis. Mycobacterium tuberculosis. Mycobacterium tuberculosis. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KW Tobecoulosis, therapy; vaccine; numunogen; ss. KX XX XX XX XX XX XX XX XX X
1 1 1 1 1 1 1 1 1 1		TIGGAACAGCTGGCCGCAGGCGGGGGCACCAGGCCTTGCAACAGGGGCACCAGGCCTTGGAGGGGCACCAACGGGAGAGCGCGATCGGCCGATCGGAGGGCACCAGGCCTGTTGTTTGT

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This DNA sequence includes a coding region for a recombinant Wycobacterium tuberculosis tri-antigen fusion protein (see ANY32059), termed Mtb32A, composed of the antigens Ral2, TbH9 and Ra35. The DNA is useful for the recombinant production of the fusion protein. Coding sequences for the antigens were modified by PCR in order to facilitate their fusion and subsequent expression of the fusion protein. 3 Coding sequences for Ral2, TbH9 and Ra25 were ligated to encode Mtb32A. The invention provides fusion proteins (see AAY32059-71) containing at least invention provides fusion proteins (see AAY32059-71) containing at least coding them are useful as vaccines for preventing tuberculosis encoding them are useful as vaccines for preventing tuberculosis (claimed). For diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein components
                                                                                                                                                                                                                         New fusion proteins useful for diagnosis, prevention and treatment tuberculosis.
                                                                                                                                                                                                                                                                                            Example; Fig 1A-B; 83pp; English
  98US-00056556.
98US-00223040.
                                                                                                             Skeiky YAW, Alderson
                                                                                                                                                      WPI; 1999-601610/51.
P-PSDB; AAY32059.
                                                                (CORI-) CORIXA CORP.
07-APR-1998;
30-DEC-1998;
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Sequence 2287 BP; 374 A; 723 C; 805 G; 382 T; 0 U; 3 Other;

; 0 Score 2266.4; DB 2; Length 2287; Pred. No. 0; 0; Mismatches 11; Indels Query Match
Best Local Similarity 99.5%;
Matches 2276; Conservative

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ATTCTCCGGCAGCCGGCGATATCGCCCCGCCGCCTTGTCGCAGGACCGGTTCGCCGACT GGGCCGGTGGTGTGTGTGTGTGTGTTCCGCCGCGACCCTATGTGATGCCGC 1561 1621

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                                                                                         97US-00818112.
97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
                                                                                                                                                                                                                                                                                                                                 Example, Fig 1; 62pp; English
                                                                    99US-00287849
                                                                                                                                                           REED S G.
SKEIKY Y A.
DILLON D C.
ALDERSON M.
                                                                                                                                                                                                                              Skeiky YA,
                                                                                                                                                                                                                                                    WPI; 2002-171134/22.
P-PSDB; AAU74588.
                        US2002009459-A1
                                                                                         13-MAR-1997;
01-OCT-1997;
18-FEB-1998;
                                                                    07-APR-1999;
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                                             24-JAN-2002
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(CAMP/)
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ATTCTCCGGCAGCCGGCGATATCGCCCCGCCGGCCTTGTCGCAGGACCGGTTCGCCGACT 1680
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/transl_except= (pos:597. .605, aa:Ala-Gln)
/transl_except= (pos:798. .802, aa:Ala)
/note= "This codon has an apparent 2 nucleotide insertion
                                                                                                                                    1801 Arcccaacegrercerercaacaacaacacereacegececececeaceare
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                                  ACATCAACACCAAACTGGGCTACAACAACGCCGTGGGCCCCGGGACCGGCATCGTCATCG
                                                                                ATCCCAACGGTGTCGTGCTGACCAACACCACGTGATCGCGGGCGCCCCCACCGACATG
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                     TCCCCGCGCTGCCCCTCGACCCGTCCGCGATGGTCGCCCAAGTGGGGCCCACAGGTGGTCA
                                                                                                                                                           CGTTCAGCGTCGGCTCCGGCCAAACCTACGGCGTCGATGTGGTCGGGTATGACCGCACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein; tuberculosis; Mycobacterium tuberculosis; gene; ds;
tuberculostatic; immunogen; vaccine; Mtb32-Mtb39; Ra12; TbH9; Ra35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding antigenic fusion protein Ral2-TbH9-Ra35 (Mtb32-Mtb39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   '*tag= a
'product= "Mtb32-Mtb39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 42. .2231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK14128 standard; DNA; 2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCGAAA 2287
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08-MAY-2002
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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents DNA encoding an M. tuberculosis fusion protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion proteins of Mycobacterium tuberculosis antigens, useful for diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTAGAAATAATTTTGTTTACTTTAAGAANGANATATACATAGCATCACCATCACCATC
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TTCATGGTGGATTTCGGGGCGTTACCACCGGAGATCTACGCGGGGATGTACGCCGGC TTCATGGTGGATTTCGGGGCGTTACCACCGGAGATCACTCCGCGAGGATGTACGCCGGC

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TITICGGCCGCGTCGGCGTITICAGTCGGTCTGGGGTCTGACGGTCGGGGTCGTGGATA

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Location/Qualifiers
1. .2190
                                                                                                                   Disclosure, Fig 6; 39pp, English
                                                     06-OCT-2000; 2000WO-US027652
                                                              99US-0158585P
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ilarity 99.9%;
Conservative
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Best Local Similarity
Matches 2188; Conserv
                                                                                           P-PSDB; AAO22142
                                     WO200125401-A2
    Unidentified.
Chimeric.
                                                              07-OCT-1999;
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ACGCCGTAYGGCTGACGGTGCCCCCGCCGGTGATCGCCGGAACCGTGCTGAACCTGAACCTGATG

ACGGCGTATGGGCTGACGGTGCCCCCGGTGATCGCCGAGAACCGTGCTGAACTGAACTGATG

ATTCTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGCGATCGCGGTCAACGAGGCC GAATACGGCGAGATGTGGGCCCCAAGACGCCGCCGCGATGTTTGGCTACGCCGCGGCGACG

822 ATTCTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGCGATCGCGGTCAACGAGGCC

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/*tag= a /product= "Ral2-H9-32A fusion protein"

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 (State of C-terminal fragment of serine protease antigen MTB32A of MTB32A of Exterminal Fragment of serine protease antigen MTB32A of MYCobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both waryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence. Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

Sequence 2191 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 1 Other;

GTGCCGCAGGCCTGGGCCGCGGCCAACCAGGCAGTCACCCCGGCGGCGCGGGCGCTGCCG 1481 1141 AACATGGTGTCGATGGCCAACAACAACCACATGTCGATGACCAACTCGGGTGTGTGGATGACC GGGCTCCTCGAGCAGGCCGCCGCGGTCGAGGAGGCCTCCGACACCGCCGCGGCGAACCAG 1021 TTGATGAACAATGTGCCCCAGGCGCTGCAACAACTGGCCCAGGCCCAGGGACCACG ACCGCGCGCAAAACGGGGTCCGGGCGATGAGCTCGCTGGGCAGCTCGCTGGGTTCTTCG GGGCTCCTCGAGCAGGCCGCCGCGGTCGAGGAGGCCTCCGACACCGCCGCGGCGAACCAG TTGATGAACAATGTGCCCCAGGCGCTGCAACAGCTGGCCCCAGCCCAGGGCAGGGCACGACG CCTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCGCCATCGGTCGCCGATCAGC cerretricasacirecirescristasasasecerrescerescristases ACCGCGGCGCAAAACGGGGTCCGGGCGATGAGCTCGCTGGGCAGCTCGCTGGGTTCTTCG AACACCTTGAGCTCGATGTTGAAGGGCTTTGCTCCGGCGGCGGCCGCCCAGGCCGTGCAA 1062 1122 1081 1201 1302 1002 1182 1242 1261 1321 1422 961 1362 δ 셤 ò a à . <u>G</u> <u>P</u> P · à 8 · 성 - 8 q 101 161 120 221 180 281 341 AACAACGGCAACGCCACGAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTC 240 9 ATGCATCACCATCACCATCACAGCGGCGGTCCGATAACTTCCAGGTGTCCCAGGGTGGG 121 GGGGGTCACCCACCGTTCATATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGAC GGCATCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACC 241 GGCATCTCCACCGGCGACGTGATCACCGCGTCGGTCGACGGCGCTCCGATCAACTCGGCCACC GGGGGGTCACCCATCCATATCGGGCCTACCGCCTTCCTCGGCTTTGGGTGTTGTCGAC ATGCATCACCATCACCATCACGCCCCCCTCCGATAACTTCCAGCTGTCCCAGGGTGGG CAGGGATTCGCCATTCCGATCGGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGT AACAACGGCAACGCGCACGAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTC Score 2187.4; DB 4; Length 2191; Pred. No. 0; 1; Mismatches 2; Indels 0;

1301 1260

" MTB72F-DPV (fusion MTB81F) protein"

/product=

WO2003070187-A2 28-AUG-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                          1741 GGGACCGGCATCGTCATCGATCCCAACGGTGTGCTGCTGCTGCCAACAACAACACGTGATCGCG
                                                                                                                                                                                                                                                                                                                                                                         1921 CCGTCGCCGCGATCGGTGGCGCGTCGCGGTTGGTGAGCCCGTCGTCGTCGCGATGGGCAAC
                              GIGGGGCAGAIGGGCCCCAGGGCCCGGTGGTGCTTGCTGCTGCTGCTGCTTCCGCCG
                                                                                                             1602 GACCCTATGTGATGCCGCATTCTCCGGCAGCCGGCGATATCGCCCCCGCCGGCCTTGTCG
                                                                                                                                                     CAGGACCGGTTCGCCGACTTCCCCGCGCTGCCCCTCGACCCGTCCGCGATGGTCGCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCGTGCAGGCGTCGGATTCGCTGACCGGTGCCGAAGAGACATTGAACGGGTTGATCCAG
                                                                                                                                                                       1621 caddaccadriceccadacriceccacacriceccricarccerecarageresecaa
                                                                                                                                                                                            GTGGGGCCACAGGTGATCAACACCCAAACTGGGCTACAACAACGCCGTGGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium MTB72F-DPV (fusion MTB81F) protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGTCGGTATGAACACGGCCGCGTCCTAGG 2232
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB99 attigen, or MTB32A, MTB39 and MTB95A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.

Sequence 2451 BP; 389 A; 785 C; 870 G; 407 T; 0 U; 0 Other;

New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB33 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.

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Reed

Guderian J,

Skeiky Y,

WPI; 2003-697554/66. P-PSDB; ADA26367.

15-FEB-2002; 2002US-0357351P.

(CORI-) CORIXA CORP.

18-FEB-2003; 2003WO-US004903

Claim 84; Fig 8; 112pp; English.

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121 GGTGGGGGGTCACCCACCGTTCATATCGGGCCTACCGCCTTCCTCGGCTTGGGGTGTTGTC 180
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                                                                                                                                                                                                                                                                       99 GGGCAGGGATTCGCCATTCCGATCGGGCGATGGCGATCGCGGGCCAGATCCGATCG
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                                                                                                                                   39 CATATGCATCACCATCACCATCACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGT
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95.6%; Score 2186.8; DB 8; Length 2451; 99.9%; Pred. No. 0; ive 0; Mismatches 2; Indels 0;
                                Best Local Similarity 99.9
Matches 2188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
tuberculosis; tuberculostatic; gene therapy; vaccine.
1621 TCGCAGGACCGGTTCGCCGACTTCCCCGCGCTGCCCCTCGACCCGTCCGCGATGGTCGCC
                                                                                       1681 CAGTGGGGCCACAGGTGGTCGACATCAACACCAAACTGGGCTACAACAACACGCCGTGGGC
                                TCGCAGGACCGGTTCGCCGACTTCCCCGCGCTGCCCCTCGACCCGGTCGCGATGGTCGCC
                                                                         CAAGTGGGGCCACAGGTGGTCAACATCAACACCAAAACTGGGCTACAACAACAAGGCGGTGGGC
                                                                                                                   1741 GCCGGGACGGCATCGTCATCGATCCCAACGGTGTCGTGCTGACAACAACAACAACGTGTC
                                                                                                                                                           1839 GCGGGGGCACCGACATCAATGCGTTCAGCGTCGGCTCCGGCCAAACCTACGGCGTCGAT
                                                                                                                                                                         1801 GOGGCGACCGACCATCAATGCGTTCAGCGTCGGCTCCGGCCAAACCTACGGCGTCGAT
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                                                                                                                                                                                                                                                             CTGCCGTCGGCGCGATCGCTGCGCGCGTCGCGGTTGGTGATGATCGTCGTCGTCGTCGCGATGGGC
                                                                                                                                                                                                                                                                                                                                               2041 CAAACGTGCAGGGTCGGATTCGCTGACCGTGCCGAAGAGACATTGAACGGGTTGATC
                                                                                                                                                                                                       GIGGICGGGIATGACCGCACCAGGATGICGCGGTGCTGCAGCTGCGCGCGGTGCC
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New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.

English. 84; Fig 7; 112pp; Claim

The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, with WTB32A, MTB32A and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.

Sequence 2487 BP; 394 A; 784 C; 896 G; 413 T; 0 U; 0 Other;

540 638 698 99 218 420 518 480 578 009 158 120 180 278 240 338 CTCGGCATCTCCACCGGCGACGTGATCACCGCGGTCGACGCGCTCCGATCAACTCGGCC 300 ACCGCGATGGCGGACGCGTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGG 398 360 CAAACCAAGTCGGGCGCGCGTACAGGGAACGTGACATTGGCCGAGGGACCCCGGGCC 458 98 9 CTGTTTTCGGCCGCGTCGGCGTTTCAGTCGGTGGTCGTCGGGGGTCTGACGGTGGGGTCGTGG CAAACCAAGTCGGGGGGGGCACGCGTACAGGGAACGTGACATTGCCGAGGAACCCCGGGCC GAATTCATGGTGGATTTTCGGGGCGTTACCACCGGAGATCAACTCCGCGAGATGTACGCC GECCCGGGTTCGGCCTCGCTGGTGGCCGCGCGCTCAGATGTGGGGACAGCGTGGCGAGTGAC CTGTTTTCGGCCGCGTCGGCGTTTCAGTCGGTGTCTGGGGTCTGACGGTGGGGTCGTGG ATAGGTTCGTCGGCGGGTCTGATGGTGGCGGCGCCTCGCCGTATGTGGCGTGGATGAGC GAATTCATGGTGGATTTCGGGGGCGTTACCACCGGAGATCAACTCCGCGAGGATGTACGCC GGTGGGGGGTCACCCACCGTTCATATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTC GETGGGGGGTCACCCCACCGTTCATATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTC GACAACAACAACGGCAACGGCACGAGGCCTGGTGGTCGGGGGGCGCTCCGGGGGGAAGT cressearcresacesegaesarcacesegaesacesegececrecearcaacressee GGGCAGGGATTCGCCATTCCGATCGGGCGAGGCGATGGCGATCGCGGGCCAGATCCGATCG Gaps ; 0 DB 8; Length 2487; 2; Indels Query Match 95.6%; Score 2186.8; Best Local Similarity 99.9%; Pred. No. 0; Matches 2188; Conservative 0; Mismatches 541 19 241 339 301 399 361 459 519 481 579 639 601 39 Н 66 159 121 219 181 279 421 6 B 6 8 6 Dp 8 8 g 8 8 8 · 6 장염 g g 8 정 à d

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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymeclotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                         Query Match 95.6%; Score 2186.8; DB 8; Length 2637; Best Local Similarity 99.9%; Pred. No. 0; Matches 2188; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                               Sequence 2637 BP; 428 A; 840 C; 928 G; 441 T; 0 U; 0 Other;
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GCCGGGACCGGCATCGTCATCGATCCCAACGGTCTCGTGCTGACCAACAACCCGTGATC 1838 2018 1560 CCGCGACCCTAIGIGATGCCGCAITCTCCGGCAGCGGCGATATCGCCCCGCCGGCCTTG 1658 1680 CAAGTGGGGCCACAGGTGGTCAACATCAACAACCAAAACTGGGCTACAACAACGCCGTGGGC 1778 GCGGCCCACCGACATCAATGCTTCAGCGTCGCCTCCGGCCAAACCTACGGCGTCGAT 1898 1478 1440 1538 1500 1598 TOGOAGGACOGGITOGCOGACTICCCCGGGCTGCCCTCGACCCGTCGGGATGGTCGCC 1718 GIGGICGGGIAIGACCGCACCCAGGAIGICGCGGGGCTGCAGCTGCGGGTGCCGGTGGC 1958 1118 1080 1178 1140 1238 1200 1298 1260 1358 1320 1418 1380 GGTGGGGTCCTCGAGCAGGCCGCGCGGGGGTCGAGGAGGCCTCCGACACGCGCGGGGGGAAC 1058 GETGGGCTCCTCGAGCAGGCCGCCGCGGTCGAGGAGCCTCCGACACGCCGCGGCGAAC 1020 900 966 960 CTGCCGTCGGCGGCGATCGGTGGCGGCTCGCGGTTGGTGAGCCCCGTCGTCGCGATGGGC CCGCTGACCAGCCTGACCAGCGCGGGAAAGAGGGCCCGGGCAGATGCTGGGCGCGGCTG TCGCAGGACCGGTTCGCCGACTTCCCCGGGCTGCCCCTCGACCGGTCGCGCATGGTCGCC CAGITGATGAACAATGTGCCCCAAGCGCTGCAACAGCTGGCCCAGCCCACGCAGGGCACC 1081 ACGCCTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCGCATCGGTCGCCGATC AGCAACATGGTCGATGGCCAACAACAACATGTCGATGACCAACTCGGGTGTGTCGATG 1261 CAAACCGCGCGCAAAACGGGGTCCGGGGCGATGAGCTCGCTGGCTCGCTGGCTCGTTCT TOGGTGCCGCAGGCCTGGGCCGCGGCCAACCAGGCAGTCACCCCGGCGGCGCGCGGCGCCTTG COGCTGACCAGCCTGACCAGCGCCGCGGAAAGAGGGCCCCGGGCAGATGCTGGGCGGCTG cogengagacacacagacacagacacagacagacacagacacagacacagacacagacacagacaca GCCGAATACGGCGAGATGTGGGCCCCAAGACGCCGCGCGATGTTTGGCTACGCCGCGGCG ACGCCTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCGCATCGGTCGCCGATC GCCGAATACGGCGAGATGTGGGCCCAAGACGCCGCCGCGATGTTTGGCTACGCCGCGGCG ACGGCGACGGCGACGTTGCTGCCGTTCGAGGAGCGCCCGGAGATGACCAGCGCG 1501 1561 1659 1621 1719 1681 1779 1741 1839 1801 1899 1861 1959 1479 1441 1539 1599 1059 1021 1119 1179 1141 1239 1201 1299 1359 1419 901 999 961 841 939 879

New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis. Location/Qualifiers
4. .2796
4. .7796
7+tag= "Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f) fusion protein" Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f)-fusion DNA: Vaccine; immunity; diagnostic agent; gene therapy; MIB72F; MAPS; chimeric; gene; ds. CAGGTGGTCGGTATGAACACGGCCGCGTCC ٦ .. Guderian 13-MAR-2002; 2002WO-US008223. 13-MAR-2001; 2001US-0275837P. AAD47110 standard; DNA; 2808 (revised)
(first entry) Skeiky Y, Brannon M, WPI; 2002-759844/82. P-PSDB; AAE29731. (CORI-) CORIXA CORP. ŝρ. Mycobacterium s Leishmania sp. Chimeric. WO200272792-A2 29-AUG-2003 27-JAN-2003 19-SEP-2002 AAD47110; 2161 8 8

CAGGIGGICGGIAIGAACACGGCCGCGICC 2228

2199

AACAGCGGTGGGCAGGCGCGAAACGCCCCGTGCGGGCCTGGCAGGTGGTCGCGCTCGGC

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P ò g δ g ò The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are

Example 6; Page 128-129; 155pp; English.

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useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mycobacterium sp. MTB72F-Leishmania sp. thiol specific antioxidant [TSA, MAPS (ake 1951)] fusion DNA. This sequence comprises Mycobacterium sp. MTB72F (a 72 kDa poly-protein fusion construct comprising Ral2-TbH9-Ral5) linked to the Leishmania TSA (MAPS). (Updated on 29-AUG-2003 to standardise OS field)	Sequence 2808 BP; 466 A; 889 C; 982 G; 471 T; 0 U; 0 Other;	Nuery Match 95.6%; Score 2186.8; DB 6; Length 2808; Set Local Similarity 99.9%; Pred. No. 0; latches 2188; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	39 CATATGCATCACCATCACACAGGCGCGCGTCCGATAACTTCCAGCTGTCCCAGGGT 98 	99 GGGCAGGGATTCGCCATTCCGATCGGCCAATGGCCAATCGCGGCCAGATCCGATCG 158	159 GGTGGGGGGTCACCCACCGTTCATATCGGGCCTACGCCTTCCTCGGCTTGGGTGTTGTC 218	219 GACAACAACGGCGAAGGCGCACGAGGCGTGGTGGTGGGAGGCGCTCGGGGGGAAGT 278 	279 CTCGGCATCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCC 338	339 ACCGCGAIGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGG 398	399 CAAACCAAGTCGGGCGCACGCGTACAGGAACGTGACATTGGCCGAGGGACCCCCGGCC 458 	459 GAATTCATGGTGGATTTCGGGGGGTTACCACCGGAGATCAACTCCGGGAGGATGTACGCC 518 	519 GGCCCGGGTTCGGCCTGGTGGCCGGGCTCAGATGTGGGAACAGCGTGGCGAGTGAC 578 	579 CIGITITCGGCCGCGTCGGCGTTTCAGTCGGTGGGGTCTGAGGTCGGGGGTCGTGGGGGGTCGTGGGGGGTCGTGGGGGGTCTGTGTTTTCGCCGGCGTTTCAGTCGGTGGTCTGGGGTCTGAGGGTCTGAGGGTCTGAGGGTCTGAGGGTCTGAGGGGTCTGACGGTGGGGGTCGGGGGTCTGACGTGGGGGTCGGGGGGTCTGACGGTGGGGGTCGGGGGGTCTGACGGTGGGGGTCTGACGGTGGGGGGTCGGGGGGTCTGACGTGGGGGTCGGGGGGTCGGGGGGTCGGGGGGGTCGGGGGG	639 ALAGGITCGICGGGGTCTGARGGTGGCGGCGGCCTCGCCGTATGTGGCGTGGALGAGC 698 	699 GTCACCGCGGGGCAGGCCGAGCTGACCGCCCGGGTTGCTGCGGGCGCGCCTAC 758	759 GAGACGGCGTAIGGGCTGACGGTGCCCCGCCGGCGGAACCGTGAACTG 818 	819 AIGATICIGAIAGCGACCAACCICTIGGGGAAACACCCCGGGGAICGCGGICAACGAG 878

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cul as vaccines to elicit protective immunity against pathogenic coorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion peptides are used for enhancing the expression of polynucleotides, as	λ _o q _o	879 GCCGAATACGGCGAGATGTGGGCCCCAAGACGCCGCGCGATGTTTGGCTACGCCGGCGGC 938
All the invention is used in gene therapy. The present sequence is beatterium sp. MTB72F-Leishmania sp. thiol specific antioxidant [TSA, 5] data r95f.] fusion DNA. This sequence comprises Mycobacterium sp. 72 th and the sequence comprises Mycobacterium sp.	& A	939 ACGGCGACGGCGACGTTGCTGCCGTTCGAGGAGGCGCCGGAGATGACCAGCGCG 998
for a 12 August procedur rusion construct comprising Raiz-TbH9-Rais) adardise Os field) adardise Os field)	ò 8	999 GGTGGGCTCCTCGAGCGCCGCGGGTCGAGGAGCCTCCGACACCGCCGCGGCGAAC 1058
fatch 2005 DF; we A; may C; yez G; 4/1 1; 0 U; 0 Other; fatch alth 95.6%; Score 2186.8; DB 6; Length 2808; cal Similarity 99.9%; Pred. No. O; 3.2188; Conservative 0; Mismatches 2; Indels 0; Gans 0;	ठ व	1059 CAGTIGALGAACAAIGIGCCCCAGGGGCTGCAACAGCTGGCCCAGGCAGGCACC 1118 1021 CAGTIGALGAACAAIGIGCCCCAGGCGCTGCAACAGCTGGCCCAGGCCCAGGCACGCAGGCACC 1080
ATGCATCACCATCACCATCACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGT 98	장 · 음	1119 ACGCCTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCGCATCGGTCGCCGATC 1178
	λο qα΄	1179 AGCAACATGGTGTCGATGGCCAACACACATGTCGATGACCAACTCGGGTGTGTGGATG 1238
	A 42	1239 ACCAACACCTTGAGCTCGATGTTGAAGGGCTTTGCTCCGGCGGCCGCCGCCAGGCCGTG 1298
	Qy Op	1299 CAAACCGCGCGCAAAACGGGTCCGGGCGATGAGCTCGCTGGCTG
	y d	1359 TCCGGTCTCGGCCGTGGCGTGGCCGCCAACTTGGGTCGGCGGCCTCGGTCGG
ACGGCATGGCGACGCGCTTAACGGCATCATCCCCGGTGACGTCATCTCGGTGACCTCG	S S	1419 TCGGTGCCGCAGGCCTGGCCGCGCCCAACCAGGCAGTCACCCCGGGGCGCGGGGCGCTG 1478
CAAACCAAGTCGGCGCACGCGTACAGGAACGTGACATTGGCCAGGGACCCCGGCC	Š G	1479 CCGCTGACCAGCCTGACCAGCGCCGCGAAAGAGGCCCCGGCACATGCTGGGCGGGC
GAATTCATGGTGGATTTCGGGGCGTTACCGGGAGATCAACTCCGCGGAGGATGTACGCCCGCGAGAATTACGGGGGGGTTACCACCGGGAGATCAACTCCGCGAGGATGTACAACGAAGATCAACGAAGAACAACAACAAACA	ठ व व	1539 CCGGTGGGGCAATGGGCCCAGGCCCGGTGGTGGCCTAATGGTGTGTGT
GGCCCGGGTTCGGCCTCGCTGGCGCGGGGCTCAATGTGGGACAGCGTGGCGAGTGGCAACGCGGGGAACGCGGGGAACGCGGGGAGTGGCGAGCTCAAATGTGGGACACAGCGTGGCCAGGTGGCGGGGGGGG	<i>장</i> 옵.	1599 CCGCGACCTATGTGATGCCGCATTCTCCGGCAGCGGCGATATCGCCCGGCCGCGCCTTG 1658
CTGTTTTCGGCCGCGTCGGCGTTTCAGTCGGTGGTCTGGGGGTCTGAGGGTCGGGGGTCGGGGGTCGGGGGTCGGGGGGGG	े ठे [.] व	1659 TCGCAGGACCGGTTCGCCGACTTCCCCGCGCTGCCCTCGACCCGTCGGCATGGTCGCC 1718
ATAGGTTCGTCGCCGGTCTGATGGTGGCGGCGCCCTGCCGTATGTGGCGGTGGATGAGCCTGCCGTATGTGGCGGTGATGAGCGGCGGCGCCTAGCGTGATGATGATGAGCGATCGAGCGCTGATGAGAGATCGTCGCGCGCG	상 염	1719 CAAGTIGGGGCCACAGGTGGTCAACATCAACAAACTGGGCTACAACAACAACGGCGTGGGC 1778
STCACCGCGGGCAGCCGAGCCGCCGCCCGGGTCCGGGTTGCTGCGGCCTAC 75	· 65 - 음	1779 GCCGGGACCGGCATCGTCGATCCCAACGGTGTCGTGCTGACCAACAACGACGGTGATC 1838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB33 antispens, with or without the MTB35A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                AACAGCGGTGGGCAGGGCGGAACGCCCCGTGCGGTGCCTGGCAGGTGGTCGCCGCTCGGC
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  Length 2808;
                                              2; Indels
DB 8;
Score 2186.8;
Pred. No. 0;
0; Mismatches
95.68;
                                            Matches 2188; Conservative
                      Similarity
Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTB85A;
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/product= "MTB72F and 85b complex (fusion MTB103F)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; gene; fusion protein; MTB32A, MTB39; antigen, MTB32A, MTB39; M
tuberculosis; tuberculostatic; gene therapy; vaccine; MTB72F; 85B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.6%; Score 2186.8; DB 8; Length 3060;
llarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches 2; Indels 0;
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P-PSDB; ADA26370.
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Best Local Similarity
Matches 2188; Conserv
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                                                                                         ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB35A;
tuberculosis; tuberculostatic; gene therapy; vaccine.
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                                                              DNA.
                                                                                                                                                                                                                               /product= "MTB72F-hTCC#1 (fusion MTB102tm2F) protein"
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                                                            Mycobacterium MTB72F-hTCC#1 (fusion MTB102tm2F) protein, encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.6%; Score 2186.8; DB 8; Length 3104; llarity 99.9%; Pred. No. 0; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3104 BP; 510 A; 968 C; 1104 G; 522 T; 0 U; 0 Other;
                                                                                                                                                                                     Location/Qualifiers
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                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberculosis infection.
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Best Local Similarity
Matches 2188; Conserv
                                                                                                                                                      Mycobacterium sp.
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                               20-NOV-2003
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1058 1020 1080 1178 1238 1260 1358 1418 1298 1320 1380 360 458 420 480 578 638 600 698 999 758 720 818 780 878 840 938 900 966 960 GAATICATGGTGGATTITCGGGGGGTTACCACCGGAGATCAACTCCGCGAGGATGTACGC 541 creminicascoscorroscontinos arcesis en creses actuales actuales en contratos actuales act GAGACGCCGTATGGGCTGACGGTGCCCCCGGCTGATCGCCGAGAACCGTGAACTG 781 AIGATICIGATAGCGACCAACCICITIGGGGCAAACACCCCGGCGATCGCGGTCAACGAG GCCGAATACGGCGAGATGTGGGCCCCAAGACGCCGCCGCGATGTTTGGCTACGCCGCGCGC 301 Accedearecedeacecedriaacecearcareceereacereacereserse CAAACCAAGTCGGGCGGCACGCGTACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 361 CAAACCAAGTCGGGCGGCGCGCGTACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC GAATICAIGGIGGAITICGGGGCGIIACCACCGGAGAICAACICCGCGAGGAIGIACGCC GGCCCGGGTTCGGCCTCGCTGGTGGCCGCGCTCAGATGTGGGACAGCGTGGCGAGTGTGAC 481 gececegerregecreeregregecececececreargages CTGTTTTCGGCCGCGTTCGGCGTTTCAGTCGGTGGTCTGGGGGTCTGACGGTGGGGTCGTGG ATAGGTTCGTCGGCGGGTCTGATGGTGGCGGCGCCTCGCCGTATGTGGCGTGGATGAGC ATAGGTTCGTCGGCGGTCTGATGGTGGCGGCCGCCTCGCCGTATGTGGCGTGGATGAGC GTCACCGCGGGGCAGGCCGAGCTGACCGCCGCCCAGGTCCGGGGTTGCTGCGGGGGGGCCTAC GAGACGGCGTATGGGCTGACGGTGCCCCCGCCGGTGATCGCCGAGAACCGTGCTGAACTG ATGATTCTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGCGATCGCGGTCAACGAG ACGGCGACGGCGACGGCGACGTTGCTGCCGTTCGAGGAGGCGCCGGGAGATGACCAGCGCG ACGGCGACGGCGACGTTGCTGCCTTCGAGGAGGCGCCGGAGATGACCAGCGC GGTGGGCTCCTCGAGCAGGCCGCCGCGGTCGAGGAGGCCTCCGACACCGCCGCGCGAAC GGTGGGCTCCTCGAGCAGGCCGCCGCGGTCGAGGAGGCCTCCGACACCGCCGCGCGGCGAAC CAGTTGATGAACAATGTGCCCCAGGCGCTGCAACAGCTGGCCCAGCCCAACAGGCACC 1119 ACGCCTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCGCATCGGTCGCCGATC ACGCCTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCCCATCGGTCGCCGATC 1179 AGCAACATGGTGTCGATGGCCAACAACCACATGTCGATGACCAACTCGGGTGTGTCGATG AGCAACATGGTGTCGATGGCCAACAACCACATGTCGATGACCAACTCGGGTGTGTCGATG Accaacaccrreagecrearerreaagecrrrecrreegecgecgecgecgecgre <u>ACCAACACCTTGAGCTCGATGTTGAAGGGCTTTTGCTCCGGCGGCGGCCCGCCAGGCCGTG</u> CAAACCGCGCGCAAAACGGGGTCCGGGCGATGAGCTCGCTGGGCTCGCTGGGTTCT 339 459 639 399 519 579 669 421 601 1059 1021 1081 1141 759 721 819 841 939 901 666 961 1239 1201 1299 1261 1359 1321 661 879 9 · 9 · 8 g. ò 8 8 . 염 8 8 6 B ු යු <u>В</u>. 장 염. 장 염. 장 음상 g ි ර

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGGCAGGGATTCGCCATTCCGATCGGCCAGCGATGGCGATGGCGGGCCAGATCCCATCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding a fusion polypeptide with the WTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 ACCGCGAIGGCGGACGCGCITAACGGGCAICATCCCGGGGAGACGICATCTCGGTGACCTCG
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                                                                  protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3474 BP; 548 A; 1131 C; 1252 G; 543 T; 0 U; 0 Other;
                                             /*tag= a
/product= "MTB72F-mTCC#2 (fusion MTB114F)
Location/Qualifiers
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P-PSDB; ADA26368.
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                            1441 CCGCTGACCAGCCTGACCAGCGCGGGAAAGAGGGCCCGGGCAGATGCTGGGCCGGGCTG
                                                                                                                                                                                1621 TCGCAGGACCGGTTCGCCGACTTCCCCGCGCTCGACCCCTCGACCCGTCGCGGATGGTCGCC
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    CCGCTGACCAGCCTGACCAGCGCCGGAAAGAGGGCCCCGGGCAGATGCTGGGCGGCTG
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Mycobacterium sp.
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Produced State

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1559 CCGCGACCTATGTGATGCGCATTCTCCGGCAGCGGGGATATCGCCCCGCGGCGTTG 1610 1561 CCGGGAGCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	RESULT 14 AAD47084 ID AAD47084 standard; DNA; 2190 BP. XX XX XD 29-AUG-2003 (revised) DT 27-JAN-2003 (first entry) XX XX XX XX XX XX XX XX XX XX XX XX XX
13 GGCCCGGGTTCGGCCTCGTTGTTGCCGCGCTCAGATGTGGGACACCTTGGCGAGTTGCGTGGAGTTGCGTGGAGTTGCGTGGAGTTGCGAGTTGCGTGGAGTTGCGAGTTGCGAGTTGCGAGTTGCGAGTTGCGAGTTGCGTGGAGTTGCAGTTGCGAGTTGCAGTTGCGAGTTGCAGTTG	1739 AGCAACATGGTGTCGATGGCCAACAACGCAATGACCAACTGGGTGTTCGATG 1238

13-MAR-2001; 2001US-0275837P.

(CORI-) CORIXA CORP

Guderian Brannon M, Skeiky Y,

2002-759844/82 P-PSDB; AAE29709 recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, or 6H polynucleotide, useful as vaccine to elicit protective immunity inst pathogenic microorganisms e.g. Leishmania and Mycobacterium against pathc tuberculosis. New M15

Disclosure, Page 92-93; 155pp; English

The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polypurcleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention creases in mathods for eliciting immune response in mammals. They are used in methods for eliciting immune response in mammals. They are used in a leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is a nimal. The invention is used in gene therapy. The present sequence is a mimal. The invention and Ralz protein from M. tuberculosis and TDH9 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;

ô Accaagrogegegegegegearcagegaacgreacarrogecegagegececegecegegaa 420 101 161 120 221 GGGGGGTCACCCACCGTTCATATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGAC 180 281 240 GGCATCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACC 341 300 GCGATGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAA 401 GCGATGGCGGACGCGTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAA 360 461 TICATGGIGGATITCGGGGCGTIACCACCGGAGAICAACTCCGCGAGGAIGTACGCCGGC 521 581 9 AACAACGGCAACGCCACGAGTCCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTC CCGGGTTCGGCCTCGCTGGTGGCCGCCGCGCTCAGATGTGGGGACAGCGTGGCGAGTGACCTG ACCAAGTCGGGCGGCACGCGTACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCCGAA cadedarrodecarrodearodecarodecarodecareceadecarodeareceare GGGGGGTCACCCATCGTTCATATCGGGCCTACCGCCTTCCTCGGCTTTGGGTGTTGTCGAC ATGCATCACCATCACCATCACACGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGG CAGGGATTCGCCATTCCGATCGGGCATGGCGATCGCGGGGCCAGATCCGATCGGGT Gaps . 0 Length 2190; Indels DB 6; 3; Score 2185.2; Pred. No. 0; 0; Mismatches 95.5%; Best Local Similarity 99.9 Matches 2187; Conservative 522 102 61 181 282 342 361 42 162 121 222 241 301 402 462 421 Match Query g 8 8 g 8 8 ò

1500 1140 1301 1260 1421 1380 1481 1440 1601 1661 1020 1121 1181 1241 1200 1361 1320 1001 1061 1541 960 540 9 761 720 821 780 881 840 941 900 641 701 GTGGGGCAGATGGGCCCCAGGCCGGTGGTGGGCTCTGCTGCTGCTGCTGCTGCGCCG TTGATGAACAATGTGCCCCAGGCGTGCAACAGCTGGCCCAGGCCCAGGGGCACCAGG dercreeccerecerecceccaacrreeercecceccecceccecceccecceccecce grassechahredececchedececedragradecrehedragradracrecerece ACGCGTATGGCTTGACGGTGCCCCCGCCGGTGATCGCCGAGAACCGTGATGATG GGGCTCCTCGAGCAGGCCGCGCGCGTCGAGGGCCTCCGACACCGCCGCGGCGAACCAG CCTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCGCATCGGTCGCCGATCAGC CCTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCCATCGGTCGTCGATCAGC AACATGGTGTCGATGGCCAACCACATGTCGATGACCAACTCGGGTGTGTCGATGACC AACACCTTGAGCTCGATGTTGAAGGGCTTTGCTCCGGCGGCGGCCCCGCCAGGCCGTGCAA AACACCTTGAGCTCGATGTTGAAGGGCTTTGCTCCGGCGGCGGCGGCCGCCCAGGCCGTGCAA ACCGCGGCGCAAAACGGGGTCCGGCGATGAGCTCGCTGGGCAGCTCGCTGGGTTCTTCG dercrese es en estado es estado estado estado estado estado estado estado estado estado estado estado estado e CCGGGTTCGGCTGGTGGCCGCGGCTCAGATGTGGGACAGCGTGGCGAGTGACCTG TTTTGGCCGCGTCGGCGTTTCAGTCGGTGGTCTGGGGTCTGACGGTGGGGTCGTGGAATA derrecreacescretaresreacescescerescerrecerareresceresareacere ACGGCGTATGGGCTGACGGTGCCCCCCGGTGATCGCCGAGAACCGTGCTGAACTGATG GAATACGGCGAAGATGTGGGCCCCAAGACGCCGCGCGATGTTTGGCTACGCCGCGGCGACG GALTACGGCGAGATGTGGGCCCCAAGACGCCGCCGCGATGTTTGGCTACGCCGCGGGGACG GCGACGGCGACGTTGCTGCCGTTCGAGGAGGCGCCGGAGATGACCAGCGCGGGT GCGACGCCGACGCGACGTTGCTTCGAGGAGGCGCCCGGAGATGACCAGCGCGGT TTTTCGGCCCCCCCCTTTCAGTCGGTCTCGGCGTCTGACCGTGGGGTCGTGGATA ACCOCCEGECAGGCCGAGCTGACCGCCCCAGGTCCGGGTTGCTGCGGCGGCCTACGAG ATTCTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGCGATCGCGGTCAACGAGGCC GGTTCGTCGGCGGGTCTGATGGTGGCGGCGCCTCGCCGTATGTGGCGTGGATGAGCGTC 1501 1081 1321 1381 1542 1602 1182 1242 1201 1302 1261 1362 1422 1482 1062 1021 1122 1141 882 901 1002 961 541 642 601 702 661 762 721 822 781 841 942 481 582 Ē,g В g ð a $\dot{\delta}$ 임 ð d δ 음 ö ద ò g ð D D 셤 d ò 8 8 8 & B 8 8 õ 셤 à 임 δ 임 8 Š

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with the tuberculosis for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and prevention of Mycobacterium infection. The fusion proteins and the prevention of Mycobacterium infection. The fusion proteins and the polymbrace are useful as diagnosis, treatment and prevention of Mycobacterium in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding mediate in a protein and patternium species MTB32RM white is a DNA encoding mediate in the invention are useful as in vivo diagnostic agents and the invention are useful as in an on-human and for raising and the sequence is a DNA encoding mediate in a protein and patternium species MTB32RM white the invention are useful as in an on-human and patternium species MTB32RM white the invention are useful as in an on-human and patternium species MTB32RM white the invention are useful as in an on-human and patternium species MTB32RM white the invention are useful as an NA encoding and management and patternium species MTB32RM white the invention are useful as an NA encoding and patternium and patternium and for raising 
                                                                                                                                                                                                                                                                                                                                                                              Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGATGGCGGACGCGTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAA 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.5%; Score 2185.2; DB 6; Length 2190; 99.9%; Pred. No. 0; tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 81; Page 108-109; 136pp; English
                                                                                                                                                                                                                                                                         Skeiky Y, Reed S, Alderson M;
                                                                                                                         20-JUN-2001, 2001WO-US019959
                                                                                                                                                                 20-JUN-2000; 2000US-00597796
01-FEB-2001; 2001US-0265737P
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                                                                                                                                                      1681 GTGGGGCCACAGGTGGTCAACATCAACACCAAACTGGGCTACAACAACAACGCCGTGGGGCCCC
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                                         CAGGACCGGTTCGCCGACTTCCCCGCGCTGCCCCTCGACCCGTCCGCGATGGTCGCCCAA
                                                                    CAGGACCGGTTCGCCGACTTCCCCCGCGCTGCCCCTCGACCCGTCGATGGTCGCCCCAA
                                                                                                                         GTGGGGCCACAGGTGGTCAACATCAACACCCAAACTGGGCTACAACAACGCCGTGGGCGCC
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/*tag= a
/*tag= a
22. .417
/*tag= b
/note= "Ra12 DNA fragment"
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/*tag= c
/note= "TbH9FL DNA fragment"
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		242 AACACCTTGAGCTCGATGTTGAAGGCCTTTGCTCCGGGGGGGG	182 AACATGGTGTCGATGGCCAACAACACATGTCGATGACCAATGCGGGTGTGTCGATGACC 		TTGA TTGA			942 GCGACGGCGACGGCACGCTGCCGCTTCGAGGAGGCGCCGGAGATGACCAGCGCGGGTT 								cceerrceec		462 TICATGGIGGATTICGGGGCGTTACCACCGG		

CGACCCTATGTGATGCCGCATTCTCCGGCGGCGACGATATCGCCCGGCGGCCTTGTCG 1661 2082 ACCGTGCAGGCGTCGGATTCGCTGACCGGTGCCGAAGAGACATTGAACGGGTTGATCCAG 1041 ACCGTGCAGGCGTCGGATTCGCTGACCGGAGCGAAGAGACATTGAACGGGTTGATCAGA GTGGTCGGTATGAACACGGCGCGTCCTAG 2231 ompleted: July 3, 2004, 17:52:08 : 910 secs

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Sequence 1, Application US/09223040

| Patent No. 654452
| GENTRAL INFORMATION:
| APPLICANT: Skeliky, Yasir
| APPLICANT: Campos-Neto, Antonio
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| TITLE OF INVENTION: and Their Uses
| TITLE OF INVENTION: and Their Uses
| TITLE OF INVENTION: 014058-009010US
| CURRENT APPLICATION UNMER: US/09/223,040
| UNMER OF SEQ ID NOS: 10
| SEQ ID NO: 10
| SEQ ID NO: 10
| LENGTH: 2287
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
OTHER INFORMATION: protein Ral2-TDH9-Ra35
NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (42): (2231)
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US-09-072-967-17

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Matches 2287; Conservative
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RESULT 2
US-09-297-849-1
IS Sequence 1, Application US/09287849
Fatent No. 6677194
GENERAL INFORMATION:
APPLICANT: Red, Steven G.
APPLICANT: Dillon, Davin G.
APPLICANT: Dillon, Davin G.
APPLICANT: Dillon, Davin G.
APPLICANT: Dillon, Davin G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Gampos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: ON UNBER: US/09/287,849
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT APPLICATION NUMBER: US 08/342,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
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PRIOR FILING DATE: 1998-04-07
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TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
FOTHER INFORMATION: Description of Artificial Sequence: tri-fusion
OTHER INFORMATION: Drotein Ral2-TDH9-Raj5 (designated Mtb32-Mtb39
OTHER INFORMATION: fusion)
NAME/KEY: modified base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: CDS
LOCATION: (42):.(2231)
LOCATION: (2220)
COTHER INFORMATION: n = g, a, c or t
NAME/KEY: CDS
LOCATION: (2220)
COTHER INFORMATION: n = g, a, c or t
US-09-287-849-1

99.9%; Score 2284; DB 4; Length 2287;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2287; Conservative 0; Mismatches
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                                                CGGCCAACCAGGCAGTCACCCCGGCGGCGCGGCTGCCGCTGACCAGCG
                                                                      ATTICTICGGCGAGCGGATATCGCCCGGCCGGCCTTGTCGCAGGACCGGTTCGCCGACT
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US-09-287-849-25
US-09-287-849-25
; Sequence 25, Application US/09287849
; Patent No. 6627198
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
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APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: DATE: 1999-04-07
CURRENT APPLICATION NUMBER: US 08/918,112
PRIOR PELING DATE: 1999-04-07
PRIOR PELING DATE: 1999-04-07
PRIOR PELING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PELING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,56
PRIOR PELING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/0223,040
PRIOR PELING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 25
LENGTH: 1797 944 GACGGCGACGCGACGTTGCTGCCGTTCGAGGAGGCGCCGGAGATGACCAGCGCGGGGTGG 1003 1063 583 643 203 763 CGCGGGGCAGCCGAGCTGACCGCCGCCCGGGTCCGGGTTGCTGCGGCGCCTACGAGAC 323 563 TICGICGGCGGGTCTGAIGGTGGCGGCGGCCTCGCCGTAIGIGGCGTGGAIGAGCGICAC 703 883 503 24 CATGGTGGATTTCGGGGCGTTACCACCGGAGATCAACTCGCGAGGATGTACGCCGGCCC GGGTTCGGCCTCGCTGGTGGCCGCGCGCTCAGATGTGGGACAGCGTGGCGAGTGACCTGTT TTGGCCGCGTCGGCGTTTCAGTCGGTGGTCTGGGGTCTGACGGTGGGGTCGTGGATAGG 204 TTCGTCGGCGGGTCTGATGGTGGCGGCCGCCTCGTATGTGGCGCGTGGATGAGCGTCAC 464 CATGGTGGATTTCGGGGCGTTACCACGGAGATCAACTCCGCGAGGATGTACGCCGGCCC 524 GGGTTCGGCCTCGCTGGTGGCCGCGCGCTCAGATGTGGGGACAGCGTGGCGAGTGACCTGTT 584 TICGGCCGCGTCGGCGTTTCAGTCGGTGGTCTGACGGTCGGGGTCGTGGATAGG CGCGGGGCAGGCGAGCTGACCGCCCCAGGTCCGGGTTGCTGCGGCGGCCTACGAGAC TCTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGCGATCGCGGTCAACGAGGCCGA 444 ATACGGCGAGATGTGGGCCCCAAGACGCCGCGCGATGTTTGGCTACGCCGCGGCGACGGC GGCGTATGGGCTGACGGTGCCCCCCCGCGGTGATCGCCGAGAACCGTGAACTGATGAT TCTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGCGATCGCGGGTCAACGAGGCCGA Query Match
77.4%; Score 1770.8; DB 4; Length 1797;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1772; Conservative 0; Mismatches 2; Indels 0; FEATURE:
COTHER INFORMATION: Description of Artificial Sequence:bi-fusion
COTHER INFORMATION: protein TDH9-Ra35 (designated Mtb59f)
NAME/KEY: CDS
LOCATION: (1) .(1791)
US-09-287-849-25 TYPE: DNA ORGANISM: Artificial Sequence g à g

GCTCCTCGAGCAGGCGGCGCGGTCGAGGAGGCCT GATGAACAATGTGCCCCAGGCGCTGGAACAACTGG	CCGCCGCGGTCGAAGGCTCCGACACCGCGCGGCGAACCAGTT 623	Oy 2144 CGATGCCGCGATCAGCCGGGGGGGGGGGGGGGGGGGGGG	
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TYPE: DNA ORGANISM: Artificial Sequence FEATURE: Best Local Similarity 99.0 Matches 1180; Conservative RESULT 4 US-09-287-849-21 584 ö g ò 셤 à g δ qq ò g ઠ 1423 1244 CACCTTGAGCTCGATGTTGAAGGGCTTTGCTCCGGCGGCGGCCCGCCAGGCCGTGCAAAC 1303 1544 GGGGCAGATGGGCGCCCAGGGCCGGTGGTGGTCTCAGTGTGTGCTGCTGCTGTTTCCGCCGCG 1603 1164 ACCCTATGTGATGCCGCATTCTCCGGCAGCGGCGATATCGCCCCGCCGGCGGCTTGTCGCA 1223 1664 GGACCGGTTCGCCGACTTCCCCGCGCTGCCCCTCGACCCGTCCGCGATGGTCGCCCAAGT 1723 1224 GGACCGGTTCGCCGCGCTCCCCGCGCTCGCCCTCGACCCGTCCGGATGGTCGCCCAAGT 1283 1724 GGGGCCACAGGTGGTCAACATCAACACTGGGCTACAACAACAACGCCGTGGGCGCCGG 1783 1784 GACCGGCATCGTCATCCATCCCAACGGTGTCGTGCTGACCAACAACCACGTGATCGCGGG 1843 1344 GACCGGCATCGTCATCGCAACGGTGTCGTGCTGACCAACAACAACGTGATCGCGGG 1403 GGCCACCGACATCAATGCGTTCAGCGTCGGCTCCGGCCAAACCTACGGCGTCGATGTGGT 1903 1404 GGCCACCGACATCAATGCGTTCAGCGTCGGCCCCAAACCTACGGCGTCGATGTGGT 1463 CGGGTATGACCGCACCCAGGATGTCGCGGTGCTGCAGCTGCGCGGTGCCGGTGCCCTGCC 1963 GTCGGCGGCGATCGGTGGCGGCGTCGCGGTTGGTGAGCCCCGTCGTCGCGATGGGCAACAG 2023 1524 GTCGGCGCGATCGGTGGCGGCGTCGCGGTTGGTGAGCCCGTCGTCGCGATGGGCAACAG 1583 CGGTGGGCAGGGCGGAACGCCCCGTGCGGTGCCTGGCAGGGTGGTCGCGCTCGGCCAAAC 2083 1584 CGGTGGGCAGGCCGAACGCCCCGTGCGGTGCCTGGCAGGGTGGTCGCGCTCGGCCAAAC 1643 CGTGCAGGCGTCGGATTCGCTGACCGGTGCCGAAGAGACATTGAACGGGTTGATCCAGTT 2143 1644 CGTGCAGGCGTCGCTGACCGGTGCCGAAGAGACATTGAACGGGTTGATCCAGTT 1703 683 624 GATGAACAATGTGCCCCAGGCGCTGCAACAGCTGGCCCAGCCCAGCGCAGGCACCCAGGCC 804 CACCTTGAGCTCGATGTTGAAGGCTTTGCTCCGGCGGCGGCGGCCGCCCCAGGCCGTGCAAC 984 GCCGCAGGCCTGGGCCGCGCGAGCCAGGCAGTCACCCCGGCGGCGGCGGCGCTGCCGCT 1184 CATGGTGTCGATGGCCAACAACAACATGTCGATGACCAACTCGGGTGTGTCGATGACCAA rendedecentedecedecedentagencesecencesregativestrances 1304 1364 2084 1424 1484 1844 1904 1964 2024 1064 DP 셤 g $\stackrel{>}{\circ}$ a ò g g g ઠે g ઠે ઠે δ à g ò d δ අ à g δ Dp δ g $\dot{\delta}$ d δ qq õ ò 셤 ò δ

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Sequence 21, Application US/09287849

| Sequence 21, Application US/09287849
| Patent No. 6627198
| General INFORMATION:
| APPLICANT: Reed, Steven G. |
| APPLICANT: Stair A.W. |
| APPLICANT: Dillon, Davin C. |
| APPLICANT: Dillon, Davin C. |
| APPLICANT: Campos-Neto, Antonio |
| APPLICANT: Campos-Neto, Antonio |
| APPLICANT: Campos-Neto, Antonio |
| APPLICANT: Campos-Neto, Antonio |
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| APPLICANT: Campos-Neto, Antonio |
| TITLE OF INVENTION: and Their Uses |
| TITLE OF INVENTION: and Their Uses |
| TITLE OF INVENTION: Antonio |
| TITLE OF INVENTION: ANUMER: US 09/02/028 |
| PRIOR FILING DATE: 1997-10-01 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR PELICATION NUMBER: US 09/025,197 |
| PRIOR PELICATION NUMBER: US 09/025,197 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-12-30 |
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| PRIOR FILIN
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SCCCGTCGTCAACGCCCTAGGACAGGT
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US-09-287-849-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.3%; Score 1172.8; DB 4; Length 1801; 99.0%; Pred. No. 6e-225; tive 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                               1764 GGTCGGTATGAACACGCCGCGTCCTAGGATAIC 1797
                                                                                                                                                                               2204 GGTCGGTATGAACACGCCGCGTCCTAGGATATC 2237
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  COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
153
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                                                              Fifth Avenue
                                                                                                                                                                         #1.30
                                                                                                                                                                                                                                                                                                                                                                                                             Score 1169; DB 3;
Pred. No. 3.7e-224;
0; Mismatches 5;
                                                                                                                                                                       Version
                                                                                                                                                                                                                             ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INPORMATION:
TELEPHONE: (206) 622-4900
                                                                                                        ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM FC Compatible
OPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                             701
                                               E: SEED and BERRY LLP
6300 Columbia Center,
                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 51.1%;
Best Local Similarity 99.6%;
Matches 1172; Conservative 0
                                                                                                                                                                                                                                                                                                                                         LENGTH: 3058 base pairs
TITLE OF INVENTION: COM
TITLE OF INVENTION: ANI
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                      Washington
                                                                                                                                                                                                                                                                                                                                                                         US-08-818-112-106
                                             ADDRESSEE: SEED
STREET: 6300 CO
CITY: Seattle
STATE: Washingt
COUNTRY: USA
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        324 GGCGTATGGGCTGACGGTGCCCCGCCGGTGATGATCGCCGAGAACCGTGCTGAACTGATGAT
                                                                                          ATACGCCGAGATGTGGGCCCCAAGACGCCGCCGCGATGTTTGGCTACGCCGCGGGGACGGC
                                           TCTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGGCGATCGCGGTCAACGAGGCCGA
                                                                                                               1004 GCTCCTCGAGCAGGCCGCCGCGGTCGAGGAGGCCTCCGACACCGCCGCGGGGGAACCAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
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US-08-818-112-106
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51.1%; Score 1169; DB 4;
Best Local Similarity 99.6%; Pred. No. 3.7e-224;
Matches 1172; Conservative 0; Mismatches 5;
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 210121.417C6
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEFRA: (206) 622-631
INFORMATION FOR SEQ ID NO: 101: SEQUENCE CHARACTERISTICS:
LENGTH: 3058 base pairs
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
TOPOLOGY: linear
US-08-818-111-101
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; Sequence 101, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
; APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Vedvick, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESCIONENCE ACCOUNTING BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STRY: Seattle
STATE: Washington
COUNTRY: Washington
COUNTRY: WSA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACCCTATGTGATGCCGCATTCTCCGGCGGCGGCCGCTA 1567
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Matches 1172; Conservative	DD GGGGTATGGGCTGACCCCCGGCGGTGATCGCCGAACTGATGA DD G91 CGGCGTATGGGCTGACCCGCCGCGAACTGATGA DD CGGCGTATGGGCCCCCCGCCGAACCCGGCCCGCCGCGCGCG	0y 1123 CTTTTCCAAGCTGGGTGGCCTGTGGAAGCGGTTCGCCGCATCGGTCGCCGATCAGCA 1181 0y 11051 CTTCTTCCAAGCTGGGTGGCCTGGAAGCGGTTCGCCGCATCGGTGCCGATCAGCA 1110 0y 1183 ACATGGTGCATGGCCAACAACCAGCAGCTGGCGGCGCGCGC
1243 ACACCTTGAGCTCGATGTTGAAGGGCTTTGCTCCGGCGGCGGCCGCCAGGCCGTGCAAA 130	TGGGCGCCAGGGCCGGTGGTGGGCTCAGTGGTGTGCTGTTCCCTGTTCCCTGTTCCCGCGCGCG	ZIP: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/09/056,556 FILING DATE: 07-ARR-1998 CLASSIFICATION: NAME: MAKI, David J. REGISTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 210121.457 RELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900 TELEPHONE: (206) 622-4900 TELEPHONE: SGO 1D NO: 106: SEQUENCE CHARACTERISTICS: LENGTH: 3058 base pairs TYPE: nucleic acid STRANDEDNESS: single TYPE: nucleic acid STRANDEDNESS: single US-09-056-556-106 Best Local Similarity 99.6%; Pred. No. 3.76-224;

0y 643 GTTCGTCGGCGGGTCTGATGGTGGCGGCCGCCTCGCCGTATGTGGCGTGGATGAGCGTCA 702	Qy 703 COGCGGGGAGCCGAGCTGACCGAGCTCCGGGGTTGCTGCGGGCGCCTACGAGA 762 Db 631 CCGCGGGGCGAGGCCGAGGCTCGCCCCCAGGTTGCTGCGGGCCTACGAGA 690	QY 763 CGGCGTATGGGCTGACGGTCCCCCCCCCGTGATCGACACACAC	823 TTCTGATAGCGACCAACCTCTTGGGGCAAAACACCCCGGGCGATCGCGGTCAACGAGGCCG 88	751 ITCIGATAGCGACCATCTIGGGGCAAAAAACCCCGGGGAAIGTTTGGCGGGGGACGG 91 883 AATACGGCGAATGTTGGGCCCAAGACGCGCGATGTTTGGCTACGCGGGGGACGG 94	SATGACCAGGGGGGGG 10 SATGACCAGGGGGGGGG 10 SATGACCAGGGGGGGG 93	1003 GGCTCCTCGAGCGGCGCGCGCGCGGGGGGGGCCTCCGACACCGCCGCGGGGAACCAGT 10	Qy 1063 TGATGAACAATGTGCCCCAGGCGCTGCAACAGCTGGCCCAGCCCAGGCACGCAGGC 1122	Qy 1123 CTTCTTCCAAGCTGGGTGGCCTGTGGAAGACGGTCTCGCCGCATCGGCGGATCAGCA 1182	Oy 1183 ACATGGTGGATGGCCAACAACAACTGTGATGACCAACTGGGGTGTGTGGATGACCA 1242 Db 1111 ACATGGTGTCGATGGCCAACAACCACATGTCGATGACCAACTGGGGGTGTGCGATGTCGATGACCA 1170	Qy 1243 ACACCTIGAGCTCGATGTTGAAGGGCTTTGCTCCGGCGGCCGCCGCCGCCGCGGTGCAAA 1302 Db 1171 ACACCTIGAGCTCGATGTTGAAGGGCTTTGCTCCGGCGGCCGCCGCCCGC	Oy 1303 CCGCGGCGCAAAACGGGGTCCGGGGGATGAGCTCGCTGGGGGGGCTCGCTC	Oy 1363 GICIGGGCGGTGGGCGCCCAACTIGGGTCGGGGGGCGTCGGTTGGTTGTTGTCGG 1422	QY 1423 TGCCGCAGCCTGGGCCCAGCCCAGCAGCAGCAGCCCCGGGGCGCGGGCCCTGCCGC 1482 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 1483 TGACCAGCCTGACCAGCGGGAAAGAGGGCCCGGGCAGATGCTGGGGGGCTGCCGG 1542	Oy 1543 TGGGGGAGATGGGCCCAGGGCCGGTGGTGCTCAGTGGTGTGCTGCGTGCTTCCGCCGC 1602	Qy 1603 GACCCTATGTGATGCCGCATTCTCCGGCGCGA 1639	RESULT 9 US-09-072-967-106 ; Sequence 106, Application US/09072967 ; Patent No. 6592877
Oy 1543 TGGGCCAGATGGGCCCAGGGCCGGTGGTCAGTGGTGCTGCTGCTGCGCGC 1602	1603 GACCTATGTGACCCCATTCTCCGGCACCGCGA 1639 1603 GACCTATGTGATGCCGCATTCTCCGGCACCGGCGA 1639 1503 GACCTATGTGATGCCGCATTCTCCGGCACCGGCGA 1639 1503 GACCTATGTGATGCCTCATTCTCCCGCCACCGGCA 1639	ALCOUNT AND THE TANK	0 4 11	; GENERAL INFORMATION: ; APPLICANT: Reed, Steven G. ; APPLICANT: Skeiky, Yasir A.W. ; APPLICANT: Dillon, Davin C.	; AFFLICANY: Campos-Neco, Antonia ; APFLICANT: Vedvick, Thomas S. ; APFLICANY: Twardzik, Daniel R. : APFLICANY: Lodes Michael J.	E SIS	9 6 5	; COUNTRY: USA ; ZIP: 98104-7092 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk	ompatible PC-DOS/MS-DOS Release #1.0, ATA:	CATION N G DATE: IFICATIC Y/AGENT	; NAME: Maki, David J.; REGISTRATION NUMBER: 31,392; REFERENCE, DOCKET NUMBER: 210121.41709; TELECOMMUNICATION INFORMATION:	E: (206) 622-4 (206) 682-603 FOR SEQ ID NO: HARACTERISTICS:	LENGTH: 3098 pairs 	1%; Score 1169; DB 4; Length 3058; 6%; Pred. No. 3.7e-224;	Valive 0; Hiskatches 5; Indels 0; Gare 8 ATTTCGGGGGGGTTACCGCGGAGATCAACTCCGCGAGGATGTACGCCGGCC 52	523 CGGTTCGCCTCGCTGCGCGCGCTCAGATGTCGCGCGCGCG	

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Fatent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WINTEN, Claire M.
APPLICANT: Trans OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
                                                                                                                                                        AATACGGCGAGATGTGGGCCCCAAGACGCCGCCGCGATGTTTGGCTACGCCGCGCGGCGACGG
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GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Reskixy, Yasir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Houghton, Raymond

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Hodes, Michael J.

APPLICANT: Hodes, Michael J.

APPLICANT: Hodes, Michael J.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: Twardzik, Daniel R.

APPLICANT: ADDRESSES: SEDD and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 0-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISCOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3058 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Washington
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Best Local Similarity
Matches 1172; Conserv
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Pred. No. 1.2e-223;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHWAN, Robert D.
APPLICANT: FLEISCHWAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCES: 24366-22007,00
FILE REPERENCES: 2436-22007,00
CURRENT APPLICATION NUMBER: U5/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOOFWARE: PatentIN Ver. 2.1
SEQ ID NO 1
LENGTH 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA

: ORGANISM: Mycobacterium tuberculosis

: OTHER INFORMATION: H37Rv

US-09-103-840A-1
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Best Local Similarity 99.6%;
Matches 1172; Conservative
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US-09-103-840A-1
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                                                                                                                                         Length 4403765;
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                                                                                                                                         Score 1169; DB 3;
Pred. No. 1.2e-223;
O; Mismatches 5;
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               TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                        Query Match 51.1%;
Best Local Similarity 99.6%;
Matches 1172; Conservative 0
                                                             CDC 1551
"n" bases a
represent
                                          FEATURE:
CTHER INFORMATION: C:
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US-09-103-840A-2
 4403765
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Length 4403765;

Indels

41.4%; Score 947.4; ,DB 3; ilarity 89.3%; Pred. No. 1.7e-179; Conservative 0; Mismatches 106;

positions throughout the sequence g

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1534646 GGTGGGGGGGTCTGATGGTGGCGGCGGCCTCGCCGTATGTGGCGTGGATGAGCGTCACCG
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                                    FEATURE:
CHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various of CHER INFORMATION: represent a, t, c or US-09-103-840A-2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                 Query Match
Best Local Similarity
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                                                                 AATACGGCGAGATGTGGGCCCCAAGACGCCGCGCGATGTTTGGCTACGCCGCGGCGACGG
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US-09-103-840A-2/C
; Sequence 2, Application US/09103840A
; Batent No. 6294328
; GENERAL INFORMATION:
    APPLICANT: PLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: TUBERCULOSIS
; FILLE REFERENCE: 24366-20007.00
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
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1532850 CCTTGCACTCGATGTTGAAGGCTTTGCTCCGGCGGCC---TCAGGCCGTGGAAACCG 1532794
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Devon C.
APPLICANT: Campos-Neto, Attonio
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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Patent No. 6290569
GENERAL INPORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos. Neto, Antonio
APPLICANT: Campos. Neto, Antonio
APPLICANT: Vadyock, Thomas S.
APPLICANT: Vadvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND ME.
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Patent No. 6294328

GENERAL INFORMATION:
APPLICANT: FIRESCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION WUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENTH: 4411529
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Pred. No. 1.5e-178;
0; Mismatches 109;
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; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1
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Best Local Similarity 89.1%;
Matches 1059; Conservative
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US-09-103-840A-1/c
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Fatent No. 633862
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Bayin C.
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: OWNIGHTEN: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS AND METHODS FOR DIAGNOSIS OF THE COMPOUNDS
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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
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6300 Columbia Center, 701 Fifth Avenue
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
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41.1%; Score 941; DB 3; Length 30
Best Local Similarity 89.0%; Pred. No. 9.4e-179;
Matches 1058; Conservative 0; Mismatches 110; Indels
                                                                                                                               ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Factorion Data:
CURRARY APPLICATION DATA:
PILING DATE: 13-YAR-1997
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 21121.411C6
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-631
INFORMATION FOR EGO ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 3027 base pairs

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STRANDEDNESS: single
                               Seattle
Washington
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US-08-818-112-110
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                                                                                                           COUNTRY:
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(without alignments)
10956.269 Million cell updates/sec
Title: US-09-597-796C-11
Sequence: 1287
Sequence: 1 tetagaaataattttgttta.....ggntgtaacaaagccggaaa 2287
Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 3163042 seqs, 2412103800 residues
Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Published Applications Nh:*

| cgn2 6/ptodata/2/pubpna/PCT NEW PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 1, Appli	Sequence 15, Appl	Sequence 1, Appli	Sequence 15, Appl	Sequence 1, Appli	Sequence 8, Appli	Sequence 7, Appli	Sequence 6, Appli	Sequence 64, Appl	Sequence 5, Appli	Sequence 11, Appl	Sequence 10, Appl	Sequence 9, Appli	Sequence 17, Appl
	ID	US-09-287-849-1	US-09-886-349A-15	US-10-359-460-1	US-10-098-732A-15	US-10-359-459-1	US-10-369-983-8	US-10-369-983-7	US-10-369-983-6	US-10-098-732A-64	US-10-369-983-5	US-10-369-983-11	US-10-369-983-10	US-10-369-983-9	US-09-886-349A-17
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ф	Query Match	99.66	99.9	99.9	9.0	ο ο ο	95.6	95.6	95.6	95.6	95.6	95.6	92.6	95.6	95.5
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ALIGNMENTS

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Sequence 1, Application US/09287849

Sequence 1, Application US/09287849

Patent No. US2002000045941

GENERAL INFORMATION:

APPLICANT: Read, Steven G.

APPLICANT: Carlos Mark

APPLICANT: Carlos Mark

APPLICANT: Carlos Mark

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APPLICANT: Carlos Mark

APPLICANT: 1999-04-07

PRIOR APPLICATION NUMBER: US 08/912,578

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	; LOCATION: (33) ; OTHER INFORMATION: n = g, a, c or t ; NAME/KEY: CDS ; LOCATION: (42) (2231)	<pre>; NAME/KEY: modified_base ; LOCATION: (2270) ; CTHER INFORMATION: n = g, a, c or t US-09-287-849-1</pre>	Query Match 99.9%; Score 2284; DB 9; Length 2287; Best Local Similarity 100.0%; Pred. No. 0; Matches 2287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ACTITAAGAANGANATATACATAGCATCACCATCACCATC 60	1000A	CGTTC 18	CGCAC 2	CGACG 30 CGACG 30	GCTTA 3	S — CS — CS — CS — CS — CS — CS — CS —	26666 48 	00100 0-100 0-100 00100			GAGC	PACGG	αο α	TCTTGGGGCAAAACACCCCGGGCGATCGCGGTCAACGAGGCCGAATACGGCGAGATGTGGG 90

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US-09-886-349A-15
US-09-886-349A-15
Sequence 15, Application US/09886349A
Publication No. US20040086523A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
TILE REFERENCE: 014058-009070US
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
OTHER INFORMATION: protein MTB72F (Ral2-TbH9-Ra35 or MTB32-MTB39
OTHER INFORMATION: fusion)
FEATURE:
NAMB/KBY: CDS
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OTHER INFORMATION: MTB72F
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NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a,
FEATURE:
NAME/KEY: modified_base
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ATCCCAACGGTGTCGTGACCAACAACCACGTGATCGCGGGCGCCACCGACATCAATG GCGCGTCGCGGTTGGTGAGCCCGTCGTCGCGATGGGCAACAGCGGTGGGCAGGGCGAAA GCGGCCTCGCCGTTGGTGAGCCCGTCGTCGCGATGGCCAACAGCGGTGGGCCAGGGCGAA CGCCCCGTGCGGTGCCTGGCAGGGGGGCGCCCCGCGAACCGTGCAGGCGTCGGATT CGGCCAACCAGGCAGTCACCCCGGCGGCGGCGGCTGCCGCTGACCAGCCTGACCAGCG CGGCCAACCAGGCAGTCACCCCGGCGGCGGGGGGGCGTGCCGCTGACCAGCCTGACCAGCCTGACCAGCG TCCCGGGCTGCCCTCGACCGGTCGGCGATGGTCGCCCAAGTGGGCCACAGGTGGTCA TCCCCGCGCTGCCCCTCGACCCGTCCGCGATGGTCGCCCAAGTGGGGCCACAGGTGGTCA ACATCAACACCAAACTGGGCTACAACAACGCCGTGGGCGCCGGGACCGGCATCGTCATCG GCCTGTGGAAGACGGTCTCGCCGCATCGGTCGCGAACAGGAGGTGTCGATGGCCAACAAGGAGGAGGAGGAGGATGGCCATCGGCCGATCGGCCGAACAGCAGTCGCGTCGCCGATCAGCAACAGGTGGTCTAGGCCAA TGAAGGGCTTTGCTCCGGCGGCGGCCGCCAGCCGTGCAACCGCGGCGCAAAACGGGG TGAAGGGCTTTTGCTCCGGCGGCGGCCGCCAGGCCGTGCAAACCGGGGCGCAAAACGGGG - 97 6 B 6 B 6 B 6 B 6 B 6 B 6 8 8 8

CGCTGACCGGTGCCGGAAGAGACATTGAACGGGTTGATCCAGTTCGATGCGCGATCCAGCCATCCAGTTGCGATGCGGGATCCAGTTGATGATCCAGTTGATCCAGTTCATCCAGTTCGATGCCGCGATCCAGC

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FILE REFERENCE: 014058-009010US
CURRENT APPLICATION NUMBER: US/10/359,459
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/223,040
PRIOR PELING DATE: 1998-12-30
NUMBER: OS SEQ ID NOS: 10
SOCTWARE: PATENTIN Ver. 2.1
LENGTH: 2287
TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
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OTHER INFORMATION: DEscription of Artificial Sequence:tri-fusion
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OTHER INFORMATION: n = g, a, c or t
FRATURE:
NAME/KEY: modified_base
1.CCATION: (33)
OTHER INFORMATION: n = g, a, c or t
FEATURE:
NAME/KEY: CDS
1.CCATION: (422)..(2231)
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NAME/KEY: modified_base
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tive 0; Mismatches
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Best Local Similarity 100.
Matches 2287; Conservative
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; Publication No. US20040013677A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and Their Uses
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	2041 CGCCCGTGCGGTGCCTGGCAGGGTGGTCGCCTCGGCCAACCGTGCAGGCGTCGGATT 2100 2041 CGCCCCGTGCGGTGCCTGGCAGGGTGGTCGCCCCCTGCCAAACCGTGCAGGCGTCGGATT 2100
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1201 ACAACCACATGTCGATGACCAACTCCGGGTGTGTCGATGACCAACACCTTGAGCTCGATGT	2281 CCGGAA 2287 2281 CCGAAA 2287
3GCGCAAAACGGGG 1320 3GCGCAAAACGGGG 1320	983-8 8, Application US/10369983
Publica Publ	<pre>// Publication No. US20030235593A1 // GENERAL INFORMATION: // APPLICANT: Skeiky, Yasir // APPLICANT: Guderian, Jeff</pre>
	APPLICANT: Reed, Steven APPLICANT: Corixa Corporation TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis FILE REPERENCE: 014058-009081US
1500	CURRENT APPLICATION NUMBER: US/10/369,983 CURRENT FILING DATE: 2003-02-18 PRIOR APPLICATION NUMBER: US 60/357,351 PRIOR FILING DATE: 2002-02-15
GGCCA 1560	DF SEQ ID NOS: 22 3: Patentin Ver. 2.1 2.8
3CCGC 1620	ficial Sequence
	INFORMATION: Description of Artificial Sequence:fusion protein INFORMATION: MTB81F (MTB72F-DPV) 983-8
1621 ATTCTCCGGCGGCGGGGGTATGTCGCCCGGCCTTGTCGCGGGCTCGCGGCTTGGGGCCGGGCT 1680 Query Match	ch . 95.6%; Score 2186.8; DB 16; Length 2451;

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AACAGCGGTGGGCAGGGGGAAGGCCCCGTGCGGTGCCTGGCAGGTGGTGGCGCTGGCGCTGGCGCTGGCGCTGGCGTGGCAGGGTGGTGGCGTGGCGTGGCAGGGTGGTGGCGTGGCCTGGCGTGCCTGGCAGGGTGGTCGCGCTCGCGCTCGGC CAAACCGTGCAGGGGTCGGATTCGCTGACCGGTGCCGAAGAGACATTGAACGGGTTGATC

CAAACCGTGCAGGCGTCGGATTCGCTGACCGGTGCCGAAGACATTGAACGGGTTGATC COGCALCCCTATGTGATGCCGCATTCTCCGGCAGCCGGCGATATCGCCCCGCCGGCCTTG TOGGAGGACOGGTTCGCCGACTTCCCCGCGCTGCCCCTCGACCGGTCCGCGATGGTCGCCCCCTCGACGACCGCGATGGTCGCCGATTCGCCGGCGCTGCCGCTCCGACGCTCGCGGATTCGCCGACTTCCCCGGCGCTGCCGCTGCCCCTCGACCCGTCGCGATTCGCCGACTCGCCGCTGCCCCTCGACCCGTGGTCGCC AGCAACATGGTGTCGATGGCCAACACCACATGTCGATGACCAACTCGGGTGTGTCGATG TOGGTGCCGCAGGCCTGGGCCGCGGCCAAGCCAGGCACTCACCCCGGCGGCGCGGCGCCTG ACGCCTTCTTCCAAGCTGGCTGGCCTGTGGAAGACGGTCTCGCCGCATCGGTCGCCGATC CAGITGAIGAACAATGIGCCCCCAGGCGCTGCAACAGCTGGCCCAGGCCCACGCAGGCACC

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2199 CAGTIGITCGTATGACAGGCCCGTCC 2228		5.10-369-983-7 Sequence 7, Application US/10369983 Publication No. US20030235593A1		obacterium Tubercu	CURRENT FILING DATE: 2003-02-18 PRIOR APPLICATION NUMBER: US 60/357,351 PRIOR FILING DATE: 2002-02-15 NUMBER OF SEQ ID NOS: 22		<pre>// ORGANISM: Artificial Sequence // ORTHOR INFORMATION: Description of Artificial Sequence:fusion protein // OTHER INFORMATION: MTB83F (MTB72F-MTI) // OTHER INFORMATION: MTB83F (MTB72F-MTI)</pre>	atch 95.6%; Score 2186.8; DB 16; Length 2487; 3181 Similarity 99.9%; Pred, No. 0; 7-3-1	CACCATCAC	CGATCG	GGTGGGGGGTGACCACCACTTCATATCGGCCCTTCCTCGGCTTGGGTGTTGTC	GACAACAACGGCAACGGGCACGAGTCCAACGCGTCGGGGAGCGCTCCGGCGGCAACT	CTCGGCATCTCCACCGCGCGCCGCTCATCACCGCGCTCCACCGCCCCCCCC	ACCECCATGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGG	CAPACCAAGTCGGGGGGGGTACAAGAAGTGATTGGGGGGGGGG	GAATTCATGGTGGATTTTGGGGGTTACAGGAACGTGACATTGGCCGAGGGATCCGGGCCCGGGCCCCGGGCCCCGGGCCCGGGCGTTACACGCGCGGGGGGTTACAGGGGATCAACAGGGAACTCGGGGGATGTACGCCCCGGGAACTCAGCGGGAACTCGGGGAACTGGAACAGCGCGCGGAATTAACAGCGAACAACAACAACAACAACAACAAACA	GCCCCGCTTCGCCTGCTGGTGGCCGCGCCTCAATGTGGGACGCGCGGAGGTGACCCCCGCGAAGGTGACCCGCGAAGGTGACGCGCGAAGGTGACGCGAAGATGTGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	

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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Glocarian, Jeffrey
APPLICANT: Glocarian, Jeffrey
TILE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TILE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TILE OF INVENTION: Heterologous Fusion Protein Constructs
TILE OF INVENTION: Heterologous Fusion
FILE REFERENCE: 014058-01201008;
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SCOFTAME: Patentin Ver. 2.1
SEQ ID NO 64
LENGTH: 2808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
CTHER INFORMATION: Description of Artificial Sequence:MTB72F-WAPS
OTHER INFORMATION: (r95f) fusion construct, TB MTB72F (Ral2-TbH9-Ra35)
OTHER INFORMATION: linked to Leishmania thiol-specific antioxidant
OTHER INFORMATION: (TSA or MAPS)
US-10-098-732A-64
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2188; Conservative 0; Mismatches
                           Sequence 64, Application US/10098732A Publication No. US20030175294A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Rederian, Jeff
APPLICANT: Rederian, Jeff
APPLICANT: Corixa Corporation
TILLE OF INVENTION: Fusion Proteins of Mycobacterium Tube;
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR APPLICATION NUMBER: US 60/357,351
SOFTWARE: Patentin Ver. 2.1
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99.9%; Pred. No. 0;
live 0; Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 2188; Conservative
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                                                                                                                    FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion
CTHER INFORMATION: MTB114F (MTB72F-mTCC#2)
US-10-369-983-9
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               60/357,351
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 3474
TYPE: DNA
CRGANISM: Artificial Sequence
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US-10-369-983-9
; Sequence 9, Application US/10369983
; Publication No. US20030235593A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Reed, Steven
; APPLICANT: Reed, Steven
; APPLICANT: Corixa Corporation
; APPLICANT: Corixa Corporation
; TILLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REFERENCE: 014658-009081US
; CURRENT APPLICATION NUMBER: US/10/369,983
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342 GCGATGGCGACCGCTTAACGGCATCATCCCGGTGACGTCTCTCGGTGACCTGGCAA 401	Qy 642 GGTTCGTCGGCGGGTCTGATGGTGGCGGCGTCGCCGTATGTGGCGTGGATGAGCGTC 701 Db 601 GGTTCGTCGGCGGGTCTGATGGTGGCGGCGCCTCGCCGTATGTGGCGTGGATGAGCGTC 660 Qy 702 ACCGCGGGGAGCCGAGCTGACCGCCCCAGGTCGGGTTGCTGCGGCGCCTACGAG 71 Db 661 ACCGCGGGGAGCCGAGCTGACCGCCCCAGGTTGCTGCGGCGCCTACGAG 72 Qy 762 ACGGCGGGAGCTGACGGTGCCCCGCCGGTGATCGCGGGCTGAACTGATG 821 Db 721 ACGGCGGTATGGGCTGACGGTGCCCCCGCGGGTGATCGCCGGTAACGATGATG 780 Qy 822 ATTCTGATAGGGTGACCAACCTTTGGGGAAACGGTGAACGATGATG 780 Qy 822 ATTCTGATAGGGCTAACGTTTTGGGGAAACGCGGGGAATGGCGGTCAACGATGATG 780		

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OTHER INFORMATION: Description of Artificial Sequence:WTB72FMutSA
OTHER INFORMATION: (Ral2-TbH9-Ra35MutSA)
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                                                                                            Length 2190;
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 0497071601371
Eax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de

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Burtjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchu
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/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a p
the genomic DNA with EcoRI and cloning
vector."
                                                                                                                     pacificus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 77.2; DB 29;
Pred. No. 0.23;
0; Mismatches 923;
                                                                                                                 /organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
                              Location/Qualifiers
1. .1628
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ilarity 40.8%;
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1717

1544

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CD937289 625 bp mRNA linear EST 15-JUL-2003 OV.106I12F010205 OV Triticum aestivum cDNA clone OV106I12, mRNA
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Triticum aestivum
Triticum aestivum
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bogrmatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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73, rue Henri Rochefort 91025 EVRY CEDEX France
7el: 33 1 69 47 54 10
7his sequence has been generated in the framework of the french
7 plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
498 AACTCCGCGAGGATGTACGCCGGCCCGGGTTCGGCTCGCTGGTGGCCGCGGCTCAGATG
                                                                                                                               1365 CIGGGCGGIGGGGIGGCCGCCAACIIGGGICGGCGGCCTCGGICGGIICGTIGICGGIG
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/organism="Triticum aestivum"
/mol_type="maxh"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="0y106112"
/tissue_type="ovary"
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Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannetr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601498
Fax: 00497071601498
Email: raif.sommer@tuebingen.mpg.de
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum.
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Organization for Nuclectide Sequencing and Analysis
C.P. 6176; Campinas, SP 13083-970, Brazil
Rel: 55 19 37881101
Fax: 55 19 37881089
Email: tebaldi@unicamp.br.
                                                                                                                                                                                                                           Indels
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Best Local Similarity 28.8%; Pred. No. 0.29;
Matches 122; Conservative 114; Mismatches 187;
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Nogueira, F.T.S., de Rosa, V.E. Jr.,
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Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bccenter.fcav.unesp.br Plate: 001 row: A column: 12 Seq primer: T7 Proncter Primer. Location/Qualifiers
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropsoneae; Saccharum.

1 (bases 1 to 611)

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
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                                                                                                                                                                                /mol_type="mRNA"
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Universidade Estadual de Campinas
Caixa Postal 610, 13083-970, Campinas SP, Brazil
Fax: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
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Matches 253; Conservative 0; Mismatches 270; Indels
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BG809984.1 GI:14180964
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Matches 401, Conservative
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                                                                                                                                                                                                                                              "Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial BCoRI digestion of Prosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's I and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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                                                                                                                                                                                                                 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   795
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                                                                                              Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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                                                           Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db xref="taxon.7227"
/clone="BACR19D16"
/clone lib="RPCT-98"
/note="end : TET3"
                                                                              Drosophila melanogaster
AL053013
AL053013.1 GI:4934461
                                                                                                                                                                                               Direct Submission
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ORGANISM
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BG809984 11516 bp mRNA linear EST 22-MAY-2001 mgct002xd11f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe grisea cDNA clone mgct002xd11f 5', mRNA sequence.

LOCUS

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/clone lib="Magnaporthe grisea Appressorium Stage cDNA" /note="Vector: pBlueScript SK(+) Vector, Site 1: EcoRI; Site_2: Xhoi, The appressorium formation-specific cDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library contains over 55,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:148305"
/clone="mgct002xd11f"
/dv_stage="Germinated conidia on apprressorium-inductive
surface"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1461 CCGGCGGCGCGCCGCTGCCGCTGACCAGCCTGACCAGCGCCGCGCGGGAAAGAGGGCCCGGG
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Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
                                                                                                                                                                                                                                Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph dean@ncsu.edu
Seq primer: T3 primer (AATTAACCCTCACTAAAGGG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.2%; Score 73.6; DB 12;
43.0%; Pred. No. 0.75;
live 0; Mismatches 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="70-15"
                                                                                                                                                              analysis
                                                                                                                                                   Construction and sequence
library in the rice blast
Unpublished (2001)
                                                                                                     1 (bases 1 to 1516)
Choi, W. and Dean, R.A.
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Pujyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (Oz-MuG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .455 GTCACCCCGGCGCGCGCGCGCTGCCGCTGACCAGCCTGACCAGCGCCGCGGAAAGAGGG 1514
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pan troglodytes DNA, clone: RP43-040E09.TJ, genomic survey
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                                                                                                                                                                                                                                                            Query Match 3.2%; Score 72.8; DB 29; Length Best Local Similarity 35.6%; Pred. No. 0.88; Matches 116; Conservative 78; Mismatches 130; Indels
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/mol_type="genomic DNA"
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/clone="BACR14N09"
/clone_lib="RPCI-98"
/note="end : T7"
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Submitted (02-UTM-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (8-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Droscophila Genome Project (BDGP). The BDGP is constructing a physical map of the Droscophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Droscophila melanogaster BAC library was prepared by Kazutoyo Osoegaw and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Droscophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, and how to order individual BAC clones, the entire library, or libraries for hybridization from the BACPAC Resource Center can be libraried to the library is not at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                         /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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                                                                                                                                                                                     3.2%; Score 72.6; DB 29;
ilarity 39.6%; Pred. No. 0.95;
Conservative 0; Mismatches 502;
                            /clone="RP43-040E09.TJ"
  'db_xref="taxon:9598"
                                                   /sex="male"
/cell_type="
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- Web: www.genoscope.cns.rx)
- Web: www.genoscope.cns.rx)
- Web: www.genoscope.cns.rx)
- Web: www.genoscope.cns.rx)
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Generics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; n bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
(bases 1 to 925)
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12.3%; Pred. No. 1;
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/db xref="taxon.7227"
/dlone="BACR19D16"
/clone=lb="RPCL-98"
/note="end : TET3"
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DEFINITION

CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit

CNS0091P/c LOCUS DEFINITION RESULT 11

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Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Direct Submission

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@qsc:riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                     Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
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1.1798
/organism="Pen troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-040F09.TJ"
                                                                                              Pan troglodytes (chimpanzee)
Pan troglodytes
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R.Site 2 : EcoRI.
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Eukaryota; Metazoa Nematoda; Chromadorea; Diplogasterida;
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Bediplogasteridae; Pristionchus.

[ bases 1 to 1956]
Srinivasaan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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/clone_lib="Ppa EcoRI BAC Library"
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the genomic DNA with EcoRI and cloning into the BAC
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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43.3%; Pred. No. 1.4;
tive 0; Mismatches 583;
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Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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( Dasses: 1 to 880)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A.; Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
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Tel: 301-838-5843
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Contact: Cathy Whitelaw
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                     Tel: 301-838-5843
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location/Qualifiers
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               BG844853 1160 bp mRNA linear EST 29-MAY-2001 1024008A08.y2 C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                     Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Bukaryota, Viridiplantae; Chlorophyta, Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 1160)
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Unpublished (2000)
Contact: Charles Hauser
                                                                                                  BG844853.1 GI:14226037
BG844853/c
LOCUS
DEFINITION
                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
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ACCESSION

REFERENCE

TITLE

JOURNAL

COMMENT

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About this library, constructed by John Davies and Jeffrey McDeamott, combines colbas from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and CDNA synthesized. The CDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBaluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with EXASSIEC (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                 Location/Qualifiers

1. 1160

/ organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
                                                                                                                                                                                                                                                              source
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GCCGCGGCCCAACCAGCCAGTCACCCCCGGCGCGCGCTGCCGCTGACCAGCCTGACC 1496 1497 AGCGCCGCGGAAAQAGGGCCCGGGCAGATGCTGGGCGGCTGCCGGTGGGGCAGATGGGC 1556 1557 GCCAGGGCCGGTGGTGGCTCAGTGGTGCTGCGTGTTCCGCCGCGCGCCTATGTGATG 1616 1617 GACTICCCCGGGGCTGCCCTCGACCGGTCGGATGGTCGCCCAAAGTGGGGCCACAGGTG 1736 1737 GICAACATCAACACCAAACTGGGGTACAACAACGCCGTGGGGCGCCGGGACCGGCATCGTC 1796 GCCAACAACACATGTCGATGACCAACTCGGGTGTGTCGATGACCAACACCTTGAGCTCG 1256 837 dereccedececcecedeceacecanaccececrecracraccecececececececece 778 718 601 CCGGGGGCCGACGGCCGGGCGCGCGCGCGCGACGCCCCCTGCGCGGCGTGGCC 1617 cogentreregecaseceses ana transces es es estados es estados es estados es 1317 GGGGTCCGGGCGATGAGCTCGCTGGCAGCTCGCTGGGTTCTTCGGGTCTGGGCGGGGG 1377 GTGGCCGCCAACTTGGGTCGGGCGGCCTCGGTCGGTTGTTGTCGGTGCCGCAGGCCTGG 957 deceaçaceerral deceaça de de constante d 1257 ATGTTGAAGGGCTTTGCTCCGGCGGCGCCCGCCAGGCCGTGCAAACCGCGGGCGCAAAAC Gaps ώ 8 Length 1160; tch 3.1%; Score 70.8; DB 12; Length al Similarity 45.0%; Pred. No. 1.8; 402; Conservative 0; Mismatches 483; Indels 1437 Query Match Best Local & Matches 403 1197 Match à

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183 CCGCCGGCGCCCCCCCCCCCCCCCCCGCGCGGGGGCCGGGCGGCGGCGG 124

2035 GCGGAACGCCCCGTGCGTGCTGGCAGGGTGGTCGCGCTCGGCCAAACCGTG 2087

Search completed: July 3, 2004, 21:56:55 Job time : 5842 secs

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tuberc

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Aduco1904 N Ada26366 N Ada26356 N Ada26351 N Ada26371 N Ada26356 N Ada26350 N Ada26368 N Ada26368 N Ada26368 N Ada26368 N

Mycobacte Mycobacte Mycobacte

Mycobacte bovis

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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen,
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skin testing; M.tuberculosis.
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             ADA26354
AA022142
                                     AAE29709
AAE1673
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AAD22636
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95US-00532136.
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96US-00658800.
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N-PSDB; AAT91432.
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05-JUN-1996;
12-JUL-1996;
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Aaw12447 Mycobacte
Aaw1680 M. tuberc
Aay32062 Mycobacte
Aay33084 M. tuberc
Aay33121 M. tuberc
Aac19706 Mycobacte
Aau4591 Antigenic
Aaw42381 Mycobacte
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Aaw43381 Mycobacte
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                                                                                              June 30, 2004, 16:39:00; Search time 27.0437 Seconds
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(c) 1993 - 2004 Compugen Ltd.
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Database :

Result

Sequence:

Title: Perfect :

Run on:

Searched:

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TbH-9. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis
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                                                                                                                                                                                                                                                                                                   TAAANQLMINIVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
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                                                                                                                                                         Gaps
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testing; M.tuberculosis.
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0
                                                                                                                           99.8%; Score 1304; DB 2; Length 263; 100.0%; Pred. No. 3.1e-105; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis antigen TbH-9
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                                                                                                                                                                                                                                                                                                                                                                                                                SVRYGHRDGGKYAXSGRRNGGPA 263
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Misc-difference 254
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DR;
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95US-00533634.
96US-00620874.
96US-00659683.
96US-00680574.
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                                                                                                                                        Best Local Similarity 100.
Matches 263; Conservative
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Vedvick TH, Twardzik
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N-PSDB; AAT91496.
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                                                                                                 Sequence 263 AA;
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22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
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                                                                                                                              Query Match
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                                                                                  A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TbH-9. The immunogenic protein, and fusion proteins containing one or more of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
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immunogenic polypeptide(s) from Mycobacterium tuberculosis - are inl in vaccines for prevention or treatment of tuberculosis, also
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                                                           Example 3; Page 126-127; 168pp; English
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97US-00818111.
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(first entry)
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Matches 263; Conservative
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09-NOV-1998
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                                                                                                                                                                                                          prevention)
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97WO-US018293
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 263 AA;
WO9816646-A2
                                                07-OCT-1997;
                                                                       11-OCT-1996;
13-MAR-1997;
                                                                                                                                                   Wedvick TS,
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                     23-APR-1998.
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Best Local S
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                                                                                                                                       Reed SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide comprises Mycobacterium tuberculosis antigen TbH-9. A DNA sequence (see AAV44371) coding for antigen TbH-9 was isolated from a N. tuberculosis strain H37Rv expression library using sera from patients having pulmonary or pleural tuberculosis. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-0CT-2003 to standardise OS
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                          New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and
                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                      Length 263;
Skeiky YAW, Dillon DC, Campos-Neto A, Houghton
, Twardzik DR, Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                      99.8%; Score 1304; DB 2; I 100.0%; Pred. No. 3.1e-105; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis immunogenic polypeptide TbH-9
                                                                                                                            Example 3; Page 125-126; 250pp; English.
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                                                                                      develop products for the diagnosis of tuberculosis.
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Best Local Similarity 100.
Matches 263; Conservative
                                    WPI; 1998-251292/22.
N-PSDB; AAV44371.
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Reed SG, Sk
Vedvick TS,
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61 İAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method inducing profective immunity against tuberculosis (TB). This sequence be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPVIAENRAELMILIAINLIGONTPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGQNTPA
                                                                                                                                                                                                                                                                                            Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used develop products for the detection of M. tuberculosis infection and f diagnosis, treatment and prevention of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                  В.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.8%; Score 1304; DB 2; Length 263; 100.0%; Pred. No. 3.1e-105;
                                                                                                                                     Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                        Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3b; Page 119-120; 230pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis antigen TbH9.
                                                                                                                                  Skeiky YAW, Dillon DC, Ca
), Twardzik DR, Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY32062 standard; protein; 263
96US-00730510.
97US-00818112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 263; Conservative
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nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEEAPEMTSAGGILEQAAAVBEASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAANOLMNNVPOALKOLAOPTOGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VAWMSVTAGGAELTAAGVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGGNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel recombinant antigens and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.8%; Score 1304; DB 2; I
100.0%; Pred. No. 3.1e-105;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide comprising antigenic portions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 160-161; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              Skeiky YAW, Dillon DC, Ca
3, Twardzik DR, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
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                                                                                                                                                                                  99WO-US003265
                                                                                                                                                                                                                                           98US-00024753.
98US-00072596.
   Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 263 AA;
                                                            WO9942118-A2
                                                                                                                                                                                                                                               18-FEB-1998;
                                                                                                                                                                                                                                                                           05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                              Reed SG, Ske
Vedvick TS,
                                                                                                                                                                                  17-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention provides fusion proteins (see AAY32059-71) containing at least 2M. tuberculosis antigens such as TBH9, e.g. ML92A, (see AAY32059) and a TBH9-TB38-1 fusion. The new fusion proteins are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or lintradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represents the Mycobacterium tuberculosis antigen TbH9. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAANQLANNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion proteins useful for diagnosis, prevention and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen; diagnosis; detection; infection; antibody; immunisation;
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100.0%; Pred. No. 3.1e-105;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto A;
   254
/note= "not identified"
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98US-00223040.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Alderson
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Best Local Similarity
Matches 263; Conserv
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 263 AA;
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                                                                                                                                                                                                           07-APR-1999;
                                                                                         WO9951748-A2
                                                                                                                                                                                                                                                                     07-APR-1998;
30-DEC-1998;
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Length 263;

M. tuberculosis

Houghton R;

Campos-Neto A, Hc I, Hendrickson RC;

9 9 120 120 180 180 240

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Mycobacterium tuberculosis, M. tuberculosis, antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
M. tuberculosis antigen TbH-9 amino acid sequence.
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Location/Qualifiers

Mycobacterium sp.

us-09-597-796c-26.rag

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. DNas encoding them, derived fusion proteins and polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX19983 to AAX19225 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLDFFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNWVSMANNHMSMTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVSMINTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
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                                                                                                                                                                                                                                                                    New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGONTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 IAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGGLLBQAAAVEEASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine; immunity; diagnostic agent; gene therapy; TbH9 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 263;
                                                                                                                                                                                        Campos-Neto A, Houghton
J, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.8%; Score 1304; DB 2; L 100.0%; Pred. No. 3.1e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 3.1 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium sp. TbH9 antigenic protein.
                                                                                                                                                                                       Skeiky YAW, Dillon DC, Ca
, Twardzik DR, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                       Example 3; Page 115; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE29706 standard; protein; 263
                                                                             99WO-US003268,
                                                                                                        98US-00025197.
98US-00072967.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention
                                                                                                                                                                                                                                          WPI; 1999-527409/44.
                                                                                                                                                           (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-2003
                                                                             17-FEB-1999;
                                                                                                                             05-MAY-1998;
               WO9942076-A2
                                                                                                                                                                                        Reed SG, Sk
Vedvick TS,
                                              26-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGGILEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.8%; Score 1304; DB 5; I 100.0%; Pred. No. 3.1e-105; iive 0; Mismatches 0;
                                                         /note= "Encoded by NAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 84; 155pp; English
                                                                                                                                                                                                                                                    Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVRYGHRDGGKYAXSGRRNGGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 263
                                                                                                                                                                                     13-MAR-2001; 2001US-0275837P
                                                                                                                                                       13-MAR-2002; 2002WO-US008223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 263; Conservative
                                                                                                                                                                                                                                                    Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                   WPI; 2002-759844/82
                                                                                                                                                                                                                      CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                    N-PSDB; AAD47081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 263 AA;
                                            Misc-difference
                                                                                          WO200272792-A2
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ID AAE17570 s
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Best Local S
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(first entry)

/label= Unknown /note= "Encoded by NAG" Location/Qualifiers

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention are treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnositic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis of an infection or monitoring of disease progression, as immunospens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species MTB39 (TDH9) protein
                                                                                                                 Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB39; TbH9 protein.
                                                                              Mycobacterium species MTB39 (TbH9) protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 83; Page 100; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky Y, Reed S, Alderson M;
                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-2000; 2000US-00597796.
01-FEB-2001; 2001US-0265737P.
                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-2001; 2001WO-US019959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-147798/19.
N-PSDB; AAD28340.
                                                                                                                                                                                                                              Misc-difference 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
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Best Local Similarity
                                                                                                                                                                         Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 263 AA;
                                                                                                                                                                                                                                                                                                           WO200198460-A2
                                        22-APR-2002
                                                                                                                                                                                                                                                                                                                                               27-DEC-2001.
    AAE17570,
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TAAANQLMMNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNWVSMANNHMSMTN 180
121 TAAANQLMINVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                                      SGVSWITHILSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA
                                       SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion proteins of Mycobacterium tuberculosis antigens, usef diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
                                                                                                                                                                                                                                              Fusion protein; tuberculosis; Mycobacterium tuberculosis;
tuberculostatic; immunogen; vaccine; TbH9-Tb38-1; TbH9; Tb38-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campos-Neto A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dillon DC, Alderson M,
                                                                                                                                                                                                                            Antigenic fusion protein TbH9-Tb38-1.
                                                                               SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                            241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                     ...r
Misc-difference 254
                                                                                                                                                     AAU74591 standard; protein; 358 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 4C-D; 62pp; English.
                                                                                                                                                                                                                                                                                                                                 /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                              97US-00818112.
97US-00942578.
98US-00025197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-00056556
98US-00223040
                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                             (revised)
(first entry)
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
CAMPOS-NETO A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-171134/22.
                                                                                                                                                                                                                                                                                                                                                   US2002009459-A1
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18-FEB-1998;
07-APR-1998;
30-DEC-1998;
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08-MAY-2002
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                                      181
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                                                                               241
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                                                                                                                                                                                                                                                                                       Chimeric
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(DILL/)
(ALDE/)
(CAMP/)
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The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protection in animals against the development of tuberculosis. The protection can among sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein of the invention. Note: The specification states that this polypeptide is encoded by the polymucleotide shown in ABK14131. (Updated on 29-AUG-2003

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0; Gaps

Length 263;

99.8%; Score 1304; DB 5; Length 20 100.0%; Pred. No. 3.1e-105; ive 0; Mismatches 0; Indels

Matches 263; Conservative

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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGGLLEQAAAVEEASD 120

1 VAWMSVTAGQABLTAAQVRVAAAAYETAYGLTVPPPVIAENRABLMILIATNILGQNTPA 60 1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA

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AAW32449
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                                                                                                                                       61 IAVNBAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                   TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                                                                                                                                                                                                        181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 240
                                                                                                                          61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                    121 TAAANOLMNNVPOALKOLAOPTOGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                                                                                                                                                                                           181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen,
                                                                                              1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunogenic polypeptide(s) from soluble M. tuberculosis antigens useful for diagnosis of M. tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                                                                               Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
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                                          Length 358;
                                      99.8%; Score 1304; DB 5; Length 3:
100.0%; Pred. No. 4.7e-105;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis antigen TbH-9FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 150-152; 190pp; English.
                                                                                                                                                                                                                                                     SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                       241 SVRYGHRDGGKYAXSGRRNGGPA 263
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DR,
                                                                                                                                                                                                                                                                                                                            AAW32381 standard; protein; 391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00523435.
95US-00532136.
96US-00620280.
96US-00658800.
96US-00680573.
                                                                                                                                                                                                                                                                                                                                                                                                                         skin testing, M.tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                     13-JAN-1998 (first entry)
                                     Query Match
Best Local Similarity 100."
Matches 263; Conservative
to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed SG, Skeiky YAW,
Vedvick TH, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-192904/17.
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                   Sequence 358 AA;
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22-MAR-1996;
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TbH-9FL The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                             133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TAAANQIMNNVPQALKQLAQPTOGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSGLGGSGGGGVAANLGRAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                          74 VAWMSVIAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 TAAANQLMINVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNIVVSMANNHMSMTN
                                                                                                                                                                                                                                                                                                                                                         1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto A, Houghton R;
                                                                                                                                                                                                                                           90.9%; Score 1187; DB 2; Length 391; 99.6%; Pred. No. 8.2e-95; ive 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis antigen TbH-9FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW32449 standard; protein; 391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky YA, Dillon DC,
I, Twardzik DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00523436.
95US-00533634.
96US-00620874.
96US-00659683.
96US-00680574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        skin testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US014674.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                     241; Conservative
                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-192903/17.
N-PSDB; AAT91521.
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                                                                                                                                                                                             Sequence 391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SV 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1996;
12-JUL-1996;
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Vedvick TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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                                                                                                                                                                                                                                              Query Match
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tuberculosis

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Sequence 391 AA;

Query Match

61

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prevention)

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This polypeptide comprises Mycobacterium tuberculosis antigen TDH-9FL. It is encoded by genomic DNA (see AAV44355) isolated from a M. tuberculosis strain H37RV genomic library using a probe from clone TDH-9 (see AAV44371). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAV64291-W64379) an immunogenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of a Soluble M. tuberculosis antigen, as well as DNA transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient bringing the spolypeptides, recombinant expression vectors and diagnostic kits for detecting M. tuberculosis infection in a patient bringing the spolypeptides, or or ligonucleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 VAWMSVTĄGQAELIPAĄQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLJGQNTPA
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 1187; DB 2;
Pred. No. 8.2e-95;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis immunogenic polypeptide TbH-9FL.
                                              Example 3; Page 133-135; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW, Dillon DC, Ca
), Twardzik DR, Lodes MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                              90.9%;
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97US-00818112.
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        diagnosis of tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 99.6
es 241, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORIF) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                        Sequence 391 AA;
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13-MAR-1997;
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Vedvick TS,
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                                                                                                                                                                                                                                                                                                                                                                                                              Onery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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                               A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TbH-9FL The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                     134 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFFEEAPEMTSAGGLLEQAAAVEEASD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
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                                                                                                                                                                                                                                                                                     Length 391;
                                                                                                                                                                                                                                                                               Score 1187; DB 2; Length 3
Pred. No. 8.2e-95;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis; infection; diagnosis; antigen; TbH-9FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis antigen TbH-9FL.
Example 3; Page 138-139; 168pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis; strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW64335 standard; protein; 391 AA.
                                                                                                                                                                                                                                                                               90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US018214
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97US-00818111
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(first entry)
                                                                                                                                                                                                                                                                                                Best_Local Similarity yy.o
Matches 241; Conservative
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3, Twardzik
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SV 242 SV 315

241

181 254

121

314

RESULT 13

17-OCT-2003 09-NOV-1998

AAW64335;

WPI; 1998-251292/22. N-PSDB; AAV44395.

(CORI-) CORIXA CORP

Reed SG, S) Vedvick TS,

07-OCT-1997; 11-OCT-1996; 13-MAR-1997;

23-APR-1998

180

253

133 120 193

9

Gaps

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This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                    74 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGGONTPA 133
                                                                                                                                                                                                                                                                                                                                                                          IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                      193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           253
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                                                    Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                            134 IAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                                                                                                                                                                                                                                                                                                                             194 TAAANQLMINIVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
                                                                                                                                                                                                                                                                                                                  1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein, Mycobacterium, primer, PCR; amplification; probe, hybridisation, detection, vaccine, immunisation, infection.
                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                            Score 1187; DB 2; Length 391;
Pred. No. 8.2e-95;
1; Mismatches 0; Indels (
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                                                                                                         Example 3B; Page 128-129; 230pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium species protein sequence
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                                                                                                                                                                                                                                                             90.9%;
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97FR-00011325.
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                                                                                                                                                                                                                                                                                        241; Conservative
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             WPI; 1998-261042/23
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Best Local Similarity
Matches 241; Conserv
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                          N-PSDB; AAV64503
                                                                                                                                                                                                                                   Sequence 391 AA;
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11-SEP-1997;
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                                                          Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression.
                                                                                                                                                                            Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
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Job time : 28.0437 secs
                                                                                                                                           Claim 32; Fig 5R; 309pp; French
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WPI; 1999-181045/15.
N-PSDB; AAX34030.
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Query Match 99.8%; Score 1304; DB 3; Length 2
Best Local Similarity 100.0%; Pred. No. 4.8e-116;
Matches 263; Conservative 0; Mismatches 0; Indels
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26 Appl
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Sequence 102, App
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Sequence 92, Appl
Sequence 91, Appl
Sequence 8, Appli
Sequence 107, App
                                                                                 June 30, 2004, 16:44:57; Search time 8.00043 Seconds (without alignments) 1697.113 Million cell updates/sec
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Sequence 25
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Copyright (c) 1993 - 2004 Compugen Ltd
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Tandzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C6
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-631
INFORMATION FOR SEQ ID NO: 91: SEQUENCE CHARACTERISTICS:
US-09-073-009-142
US-09-287-849-142
US-09-287-849-12
US-09-287-849-12
US-09-477-135A-131
US-08-311-731A-57
US-09-073-010-15
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-818-112-91; Sequence 91, Application US/08818112; Patent No. 6280969; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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Length 263;

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181 SGVSMINTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
                         61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
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NAME: MAKI, DAVId J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERICTICS:
LENGTH: 263 amino acids
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VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92, Application US/08818111
| Patent No. 6338852
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Reed, Steven G. |
| APPLICANT: Skeiky, Yasir A.W. |
| APPLICANT: Dillon, Davin C. |
| APPLICANT: Houghton, Raymond APPLICANT: Houghton, Raymond APPLICANT: Vedvick, Thomas S. |
| APPLICANT: Wardzik, Daniel R. |
| TILLE OF INVENTION: TAWACZIK, Daniel R. |
| TILLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 263;
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ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTMAEE: PS-ECHIIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
FILING DATE: 13-MAR-1997
CLASSIPICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.8e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION UNMER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.8%; Score 1304;
                                                                                                                                                                                                                                                                                                                                                     241 SVRYGHRDGGKYAXSGRRNGGPA 263
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
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LENGTH: 263 amino acids
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Matches 263; Conservative
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STREET: 6500
CITY: Seattle
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TOPOLOGY:
US-08-818-111-92
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121 TAAANQLANNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNNVSMANNHMSMTN 180
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                                                                                                     GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Byeaky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE.OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF EGUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: Mashington
COUNTRY: USA
ZIP: Washington
COUNTRY: USA
ZIP: MADDIUM TYPE: Floppy disk
COUNTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP MC compatible
CORRENT APPLICATION NUMBER: US/09/056,556
FLING DATE: 07-APR-1998
CLASSIFICATION:
CONTRY: USA
CORRENT APPLICATION:
CONTRY: APPLICATION:
CONTRY: APPLICATION:
CONTRY: APPLICATION:
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Best Local Similarity 100.0%; Pred. No. 4.8e-116;
Matches 263; Conservative 0; Mismatches 0;
Sequence 91, Application US/09056556
Patent No. 6350456
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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
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                                                    181 SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 240
                      SGVSMTNTLSSMLKGFAPPAPAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 240
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MEDIUM TYPE: Floppy disk
COMPUTER: IEN PC compatible
OPERATING SYEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%; Score 1304; DB 4; L
100.0%; Pred. No. 4.8e-116;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METITLE OF INVENTION: AND DIAGNOSIS OF
                                                                                                                                                            241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                     91, Application US/09072967
5, 6592877
                                                                                                                  241 SVRYGHRDGGKYAXSGRRNGGPA
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (206) 622-4900
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 263; Conservative
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CORRESPONDENCE ADDRESS:
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: Washington
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STRANDEDNESS: si
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ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
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121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
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                                                                                         181 SGVSMINTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGGNTPA 60
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APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.8%; Score 1304; DB 4; Length 263; 100.0%; Pred. No. 4.8e-116;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
COMPUTER: IBM FOC COMPATIBLE
COMPUTER: IBM FOC COMPATIBLE
COMPUTER: DALENTIN Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                         241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                      Sequence 92, Application US/09072596
Patent No. 6458366
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 263; Conservative
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ADDRESSEE: SEED and
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STRANDEDNESS: sir
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STATE: Washing
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US-09-072-596-92
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Sequence 8, Application US/09287849

Patent No. 6627198

GENERAL INPORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
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OTHER INFORMATION: Description of Artificial Sequence:bi-fusion OTHER INFORMATION: protein TbH9-Tb38-1
NAME/KEY: MOD_RES
LOCATION: (254)
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                                                                                                                                                                                                                     241 SVRYGHRDGGKYAXSGRRNGGPA 263
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ORGANISM: Artificial Sequence
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                                                                                 APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campoo Neto, Antonio
APPLICANT: Campoo Neto, Antonio
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 391;
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ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
TLING DATE: 13-MAR-1997
ATORNEY/AGENT INFORMATION:
NAME: MAKA, David J.
REGISTRATION NUMBER: 210121.411C6
TELEFANCE/DOCKET NUMBER: 210121.411C6
TELEFANCE/OCKET NUMBER: 210121.411C6
TELEFANCE/OCKET NUMBER: 210121.411C6
TELEFANCE (206) 622-4900
TELEFANCE (206) 682-6031
INFORMATION POR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
TENTON POR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      B: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.9%; Score 1187; DB 3; Best Local Similarity 99.6%; Pred. No. 1.1e-104; Matches 241; Conservative 1; Mismatches 0;
Sequence 107, Application US/08818112
Patent No. 6290969
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Washington
COUNTRY: USA
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US-08-818-112-107
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STREET: 630
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US-09-072-596-102
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                                                        JOS-95-818-111-102.

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90.9%; Score 1187; DB 4;
Best Local Similarity 99.6%; Pred. No. 1.1e-104;
Matches 241; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
TELEPAC: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102: SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 SV 242
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RESULT 8
US-08-818-111-102
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US-09-056-556-107
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Sequence 107, Application US/09056556

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APPLICANT: Ready, Steven G.
APPLICANT: Ready, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: Confection C.
TITLE OF INVENTION: 241

ONRESPENDENCE SEED and BERRY LLP
STREET: Steed and BERRY LLP
STREET: Mashington
COUWRRY: Washington
COUWRRY: Usa
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 391;
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                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OFRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,556

ATTONEY/AGENT INFORMATION:

NAME: Maki, David J.

ATTONEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 210121.457

TELECOMMULCATION INFORMATION:

TELEBEHONE: (206) 682-6930

TELEBEHONE: (206) 682-6931

INFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:

LUNFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:

LUNFORMATION FOR SEQ ID NO: 107:

SEQUENCE SEQUENCE SINGLE
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Fatent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
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Lodes, Michael J.
Hendrickson, Romald C.
YERVIO: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
VENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM/PC Compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
CURRENT APPLICATION NAMER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                        E. SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKA, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/09287849
Patent No. 6627198
GENERAL INFORMATION:
Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.6%
Matches 241; Conservative
               APPLICANT: Lodes, Michae APPLICANT: Hendrickson, TITLE OF INVENTION: COMP TITLE OF EQUENCES: 355 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed, Steven G.
                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
Twardzik,
                                                                                                                                                                                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                            STREET: 6300 CO
CITY: Seattle
STATE: Washingt
COUNTRY: USA
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US-09-072-967-107
                                                                                                                                           ADDRESSEE:
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US-09-287-849-26
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APPLICANT:
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90.9%; Score 1187; DB 4; Length 391;
Best Local Similarity 99.6%; Pred. No. 1.1e-104;
Matches 241; Conservative 1; Mismatches 0; Indels
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTON: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                              SOFTWARES PATENTIN Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATICN NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 107, Application US/09072967
Patent No. 6592877
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio APPLICANT: Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEO 1D NO: 102
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 391 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                            Washington
                                                                                                                                                                STREET: 6300 Co
CITY: Seattle
STATE: Washingt
                                                                                                                                                                                                                             COUNTRY: USA
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US-09-072-967-107
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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGGLLEQAAAVEEASD 120
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                                                                                       1 VAWMSVTÄGGAELTAAQVRVAAAAXETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                         121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
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                                                      Gaps
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0
Score 1187; DB 4; Length 391;
Pred. No. 1.1e-104;
1; Mismatches 0; Indels
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Campos-Neto, Antonio
Corixa Corporation
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APPLICANT:
APPLICANT:
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90.5%; Score 1182; DB 4;
99.2%; Pred. No. 8.1e-104;
iive 1; Mismatches 1;
                                      09/223,040
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 22
LENGTH: 600
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 240; Conservative
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US-09-223-040-2
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GENERAL INFORMATION:
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APPLICANT: Reed, Steven G.
APPLICANT: Steven G.
APPLICANT: Steven G.
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Fusion Protiens
TITLE OF INVENTION: And Their Uses
TITLE OF INVENTION: AND THEIR TOWNER: US 09/2187, 849
CURRENT APPLICATION NUMBER: US 08/818,112
PRIOR PILLING DATE: 1997-10-01
PRIOR PILLING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PILLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PILLING DATE: US 09/025,197
PRIOR PILLING DATE: US 09/025,197
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REPERBENCE: 014058-00902008
CURRENT APPLICATION NUMBER: US(09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR PELICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PELICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-02-18
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OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
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Patent No. 6627198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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61 IAVNEABYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGGLLEQAAAVEEASD 120 275 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 334 82 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 141 120 121 TAAANQLANNVVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNNVSMANNHMSMTN 180 202 TAAANQLAMNAVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 261 181 SGVSWTNTLSSMLKGFAPAAAAAAVOTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240 262 SGVSMINITLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVGVANLGRAA 321 61 IAVNEAEYGEMWAQDAAAMFGYAAATATATILIPFEEAPEWTSAGGILEQAAAVEEASD 1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA Gaps Gaps CTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-223-040-2 ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-22 0 Length 729; Length 600; 1; Indels Query Match 90.9%; Score 1187; DB 4; Length 6
Best Local Similarity 99.6%; Pred. No. 2e-104;
Matches 241; Conservative 1; Mismatches 0; Indels

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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Billon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa Corporation
TITLE OF INVENTION: Engion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REPERBREE: 014058-009020US
TITLE OF INVENTION: WIMBER: US 08/818,112
PRIOR FILING DATE: 1999-04-07
PRIOR PILING DATE: 1999-04-07
PRIOR PLING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR PELICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-04-07
PRIOR PLING DATE: 1998-12-30
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PRIOR PLING DATE: 1998-12-30
PRIOR PLING DATE: Patentin Ver. 2.1
SEQ ID NO 2
PRIOR PLING DATE: Patentin Ver. 2.1
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                                181 SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 240
121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                                                                                                                                 181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 274
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; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-2
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90.5%; Score 1182; DB 4; Length 729;
Best Local Similarity 99.2%; Pred. No. 8.1e-104;
Matches 240; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09287849 Patent No. 6627198
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ORGANISM: Artificial Sequence
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Search completed: June 30, 2004, 16:55:22 Job time : 8.00043 secs

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June 30, 2004, 16:52:58 ; Search time 20.5081 Seconds (without alignments) 3625.462 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1166195 segs, 282705291 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                US-09-597-796C-26
1306
                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence 12, Appl	92,	Sequence 91, Appl	Sequence 12, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 14, Appl	Sequence 102, App	Sequence 107, App	Sequence 14, Appl	Sequence 26, Appl	Sequence 20, Appl	Sequence 26, Appl	Sequence 20, Appl	Sequence 22, Appl
ΠD	US-09-886-349A-12	US-10-193-002-92	US-10-084-843-91	US-10-098-732A-12	US-09-287-849-8	US-10-359-460-8	US-09-886-349A-14	US-10-193-002-102	US-10-084-843-107	US-10-098-732A-14	US-09-287-849-26	US-09-886-349A-20	US-10-359-460-26	US-10-098-732A-20	US-09-287-849-22
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Query Match Length DB	263	263	263	263	358	358	391	391	391	391	596	596	965	965	009
Query Match	99.8	99.8	8.66	99.8	8.66	99.8	90.9	90.9	90.6	90.9	90.9	90.9	6.06	90.9	6.06
Score	1304	1304	1304	1304	1304	1304	1187	1187	1187	1187	1187	1187	1187	1187	1187
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-10-359-460	0-369-983-2	-09-886-349A-I	10-098-732A-	10-369-983-	1-369-983-2	69-983-1	0-369-6	0-369-6	1-098-732A-	0-369-6	-10-369-983-	-10-369-983-	-10-369-983-	9-983-	39-287-8	3-09-886-349A	10-359-460-2	10-098-7	10-359-459-	3-872-	US-10-193-002-106	0-084-843	0-193-002-10	0-084-	3-282-122A-6245	-10-282-12	-09-073-009-12	US-09-793-306-126	3-10-282-12	
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ALIGNMENTS

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1 VAWMSVTAGQAELIAAQVRVAAAAYETAYGLIVPPPVIAENRAELMILIATNILGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                           APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION Fusion Proteins of Mycobacterium Tuberculosis
TILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.8%; Score 1304; DB 12; Length 263; 100.0%; Pred. No. 1.1e-106; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD_RES
IOCATION: (254)
CTHER INFORMATION: Xaa = any amino acid
US-09-886-349A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Mycobacterium tuberculosis
          Sequence 12, Application US/09886349A, publication No. US20040086523A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: MTB39 (TbH9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 263; Conservative
US-09-886-349A-12
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTATION NUMBER: 31,392
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIF, 9810-4-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 91:
                                                                                                                                                                                                                                                                                                            241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                                              241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 91, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 68 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-084-843-91
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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGGILEQAAAVEEASD 120
                                                                                               61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                   SGVSMTNTLSSMLKGFAPAAAAAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
                                                                                                                                                                                      SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
                                                                                                                                                                                                                                                                                                        RESULT 2
US-10-193-002-92
Sequence 92, Application US/10193002
Sequence 92, Application US/20193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twaraik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                           TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
99.8%; Score 1304; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 263; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Maki, David J.
REGISTATION UNDERF. 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-U1-2002
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
NCE DESCRIPTION: SEQ ID NO: 92:
                                                                                                                                                                                                                              SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 92:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 263 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
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US-10-193-002-92
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      9
                                                                                                               61 IAVNEAEYGEMWAQDAAAMFGXAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                     61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLILPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                                                                                                                                                                                                                           SGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAA
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Houghton, Raymond
Vedvick, Thomas S.
Twardik, Daniel R.
Lodes, Michael R.
Lodes, Michael G.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLIPPEEAPEMTSAGGLLEQAAAVEEASD 120
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                                                                                                                                                           61 IAVNEAEYGEMMAQDAAANFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
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                                                                                                                                                                                                                                                                 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/10089732A
| Bublication No. US2000175294A1
| Bublication No. US2000175294A1
| GENERAL INFORMATION:
| APPLICANT: Skeiky, Yasir
| APPLICANT: Skeiky, Yasir
| APPLICANT: Gridan, Jeffrey
| APPLICANT: Gridan, Jeffrey
| APPLICANT: Gridan, Jeffrey
| APPLICANT: Gridan Corporation
| TITLE OF INVENTION: Heishmania Antigen
| TITLE OF INVENTION: Heishmania Antigen
| TITLE OF INVENTION: Heishmania Antigen
| FILE REFERENCE: 012010US
| CURRENT APPLICATION NUMBER: US 60/275,837
| PRIOR FILING DATE: 2001-03-13
| NUMBER OF SEQ ID NOS: 80
| SOFTHARE: Patentin Ver. 2.1
| LENGTH: 263
                                                                                        1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGQNTPA
                                                                       1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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99.8%; Score 1304; DB 14; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 263; Conservative 0; Mismatches 0; Indels 0
          Length 263;
                                        Indels
      Score 1304; DB 14;
Pred. No. 1.1e-106;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (254)
; OTHER INFORMATION: Xaa = any amino acid
US-10-098-732A-12
                                                                                                                                                                                                                                                                                                                                                      241 SVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                                 241 SVRYGHRDGGKYAXSGRRNGGPA 263
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99.8%; Scor.
100.0%; Pre
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                                Best Local Similarity 100.
Matches 263; Conservative
                            Similarity
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US-10-098-732A-12
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           Query Match
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GAPPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Billon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANTON: and Their Uses
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014059-009000S
CURRENT PAPLICATION NUMBER: US 08/942,578
PRIOR PILING DATE: 1997-10-01
PRIOR PLILING DATE: 1997-10-01
PRIOR PLILING DATE: 1998-02-18
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181 SGVSMINTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAA 240
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OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
OTHER INFORMATION: protein TbH9-Tb38-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 358;
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99.8%; Score 1304; DB 9; L
Best Local Similarity 100.0%; Pred. No. 1.7e-106;
Matches 263; Conservative 0; Mismatches 0;
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| LOCATION: (254)
| CTHER INFORMATION: Xaa = any amino acid
US-09-287-949-8
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Patent No. US20020009459A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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241 SV 242
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Sequence 8, Application US/10359460

Publication No. US2030147911A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Alderson, Mark

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

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APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

PRIOR APPLICATION NUMBER: US 09/025,197

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 46

SERO ID NOS: 46

SERO ID NOS: 46

SERO ID NOS: 86

LEWARNE: Patentin Ver. 2.1
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OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
OTHER INFORMATION: protein TbH9-Tb38-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 358;
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100.0%; Pred. No. 1.7e-106;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD_RES
LOCATION: (254)
COTHER INFORMATION: Xaa = any amino acid
MS-10-359-460-8
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ORGANISM: Artificial Sequence
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Matches 263; Conservative
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, Sequence 14, Application US/09886349A
, Publication No. US20040086523A1
, GENERAL INFORMATION:

US-09-886-349A-14

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74 VAWMSVTĄGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 133
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APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2001-02-01
SPRIOR FILING DATE: 2001-02-01
SPRIOR FILING DATE: 2001-02-01
SPRIOR FILING DATE: 2001-02-01
SPRIOR FILING DATE: 2001-02-01
SPRIOR FILING DATE: 2001-02-01
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Dillon, Davin C.
Campos-Neco, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.9%; Score 1187; DB 12; Best Local Similarity 99.6%; Pred. No. 3.8e-96; Matches 241; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7192
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 102, Application US/10193002
Publication No. US2030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: MTB39 (TbH9FL) US-09-886-349A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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; Sequence 14, Application US/10098732A; Publication No. US20030175294A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 99.6
Matches 241; Conservative
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US-10-098-732A-14
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Skeiky, Yasir A.W.
Skeiky, Yasir A.W.
Sheiky, Yasir A.W.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPUNDS OF TUBERCULOSIS
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 90.9%; Score 1187; DB 14; Length 391; Best Local Similarity 99.6%; Pred. No. 3.8e-96; Matches 241; Conservative 1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-011-2002
CLASSIFICATION: CURNOWN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAK!, David J.
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-193-002-102
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US-10-084-843-107
Sequence 107, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-631
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
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APPLICANT: Skeiky, Wasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 0.44058-0.12010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR FILING DATE: 2001-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.9%; Score 1187; DB 14; Length 391; 99.6%; Pred. No. 3.8e-96; tive 1; Mismatches 0; Indels 0
COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/084,843

FILING DATE: 25-Feb-2002

CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MARK!, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPRAX: (206) 682-6031
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                                                                                                                                                                142 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                                                                                                                                                                      202 TAAANQLAMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNNVSMANNHMSMTN
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      1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILGQNTPA
                                                       82 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNILIGQNTPA
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Publication No. US20040086523A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT PILLOMIN: Vasion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT PILLOMION NUMBER: US 09/597,796
PRIOR PLILOM DATE: 2001-06-20
PRIOR PLILMG DATE: 2000-06-20
PRIOR PLILMG DATE: 2000-06-20
PRIOR SPELICATION NUMBER: US 60/265,737
PRIOR APPLICATION NUMBER: 2001-02-01
SOFTWARE: PatentIN Ver: 2.1
SEQ ID NO 20
LENGTH: 596
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US-09-886-349A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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APPLICANT: Reed, Steven G.

APPLICANT: Reed, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Alderson, Mark

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANTON: Confess of Mycobacterium tuberculosis Antigens

TITLE OF INVENTION: and Their Uses

TITLE OF INVENTION: and Their Uses

TITLE OF INVENTION: 014058: 1999-04-07

PRIOR FILING DATE: 1999-04-07

PRIOR PLILING DATE: 1999-02-18

PRIOR PLILING DATE: 1999-04-07

PRIOR PLILING DATE: 1999-04-07

PRIOR PLILING DATE: 1999-04-07

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                                                                                                                                                                                                                                                         Length 391;
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                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                  Query Match 90.9%; Score 1187; DB 14; Best Local Similarity 99.6%; Pred. No. 3.8e-96; Matches 241; Conservative 1; Mismatches 0;
                                                                                                                         FEATURE:
COTHER INFORMATION: MTB39 full length (TbH9FL)
US-10-098-732A-14
SEQ ID NO 14
LENGTH: 391
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09287849
Patent No. US20020009459A1
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ORGANISM: Artificial Sequence
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141

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Sequence 22, Application US/09287849

Sequence 22, Application US/09287849

Patent No. US20020009459A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Corixa Corporation

TITLE OF INVENTION: and Their Uses

FILE REFERENCE: 014058-009020US

FILE REFERENCE: 014058-009020US

FILE REFERENCE: 014058-009020US

FILE REFERENCE: 014058-009020US

FURENT FILING DATE: 1999-04-07

PRIOR APPLICATION NUMBER: US 08/912,578

PRIOR PILING DATE: 1997-03-13

PRIOR PILING DATE: 1997-03-13

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-04-07

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-12-30

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TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising in TITLE OF INVENTION: Leishmania Antigen FILE REFERENCE: 014058-012010US CURRENT APPLICATION NUMBER: US/10/098,732A CURRENT FILING DATE: 2003-04-29 PRIOR APPLICATION NUMBER: US 60/275,837 PRIOR APPLICATION NUMBER: US 60/275,837 NUMBER OF SEQ ID NOS: 80 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 20 LENGTH. 596 TYPE: PATENTH SEQ ID NOS: 80 CENTRALE: PATENTH SEQ ID NOS: 80 CENTRALE: PATENTH SEQ ID NOS: 80 CENTRALE: PATENTH SEQ ID NOS: 80 CENTRALE: PATENTH SEQ ID NOS: 80 CENTRALE: PATENTH SEQ ID NOS: 80 CENTRALE: PATENTH SEQ ID NOS: 80 CENTRALE: PATENTH SEQ ID NOS: 80 CENTRALE: PATENTH SEQ ID NOS: 80 CENTRALE: PATENTH SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
OTHER INFORMATION: protein TbH9-Ra35 (designated MTB59F)
US-10-098-732A-20
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90.9%; Score 1187; DB 14; Length 596;
Best Local Similarity 99.6%; Pred. No. 6.6e-96;
Matches 241; Conservative 1; Mismatches 0; Indels 0
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US-09-287-849-22
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           RESULT 13
US-10-159-460-26
US-10-3159-460-26
IS-quence 26, Application US/10359460
PUBlication No. US20030147911A1
GENERAL INFORMATION:
APPLICANT: Read, Steven G.
APPLICANT: BAILTON: Wasir A.W.
APPLICANT: Alderson, Mark.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Haion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Haion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Haion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: BAILTON PROTICES
TITLE OF INVENTION: 10058-009020US
CURRENT APPLICATION NUMBER: US/09/287, 849
PRIOR PLING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/912,578
PRIOR APPLICATION NUMBER: US 08/912,578
PRIOR PLING DATE: 1999-04-07
PRIOR PLING DATE: 1999-04-07
PRIOR PLING DATE: 1999-04-07
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-04-07
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PRIOR PLING DATE: 1998-02-18
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Best Local Similarity 99.6%; Pred. No. 6.6e-96;
Matches 241; Conservative 1; Mismatches 0; Indels 0
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Sequence 20, Application US/10098732A
Publication No. US20030175294A1
GRNEAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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; TYPE: PRT ; ORGANISM: Artificial Sequence ; FEATURE: ; CTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-22

Query Match 90.9%; Score 1187; DB 9; Length 600; Best Local Similarity 99.6%; Pred. No. 6.7e-96; Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps

1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPEVIAENRAELMILIATNILGGNTPA 60

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Search completed: June 30, 2004, 17:14:49 Job time: 21.5081 secs

Run on:

probable pro

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70608
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, R.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Rocession: B70608
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Rocession: B70608
A;Residues: 1-391 <COL>
A;Rosidues: 1-391 <COL>
A;Rosidues: 1-391 <COL>
A;Cross-references: GB:Z93777; GB:AL123456; NID:93261726; PIDN:CAB07839.1; PID:e311073; IA;Gene: PPE
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probbale PPE protein - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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- 2004 Compugen Ltd.
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C.Species: Mycobacterium tuberculosis

C.Species: Mycobacterium tuberculosis

C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

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R,Date: 18.1 Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

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A,Accession: H70931

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A,Residues: 1-403 <a href="https://document.org/">A,Accession: H70931
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70931
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
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Best Local Similarity 43.34
Matches 117; Conservative
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C,Species: Mycobacterium tuberculosis
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C,Accession: C70568
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajundream, M. A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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A;Accession: C70568
A;Accession: C70568
A;Gerence number: A70500; MulD:98295987; PMID:9634230
A;Accession: C70568
A;Estius: preliminary; nucleic acid sequence not shown; translation not shown
A;Acsidues: 1-393 < COL.
                                    Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Reference numbering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MuID:98295987; FMID:9634230
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A;Cross-references: GB:275555; GB:AL123456; NID:g3261608; PIDN:CAA99966.1; PID:e250360; A;Experimental source: strain H37Rv
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; Pred. No. 3.9e-61;
13; Mismatches 21; Indels 5;
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Best Local Similarity 84.1%;
Matches 207; Conservative 1:
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Best Local Similarity
Matches 196; Conserv
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A;Gene: PPE
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Db 192 TAQSTLTEMITGLPNALQSLTSPLLQSS-NGPLSWLWQILFGTPNFPTSISALLTDLQPY 250 plete genome Qy 162 RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGS 221	RESULT 7 H87056 PPE-family protein [imported] - Mycobacterium leprae C;Species: Mycobacterium leppae C;Species: Mycobacterium leppae C;Species: Mycobacterium leppae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: H87056 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hamin, R.; Davies, R.M. R; Davies, R.M.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Authors: Preliminary A;Accession: H87056 A;Status: preliminary A;Molecule type: DA A;Residues: 1-421 <sto> A;Residues: 1-421 <sto> C;Genetics: A;Gene: ML182 A;Gene: ML182</sto></sto>	Sordon, S Iroyd, S. genome	RESULT 8 A70932 probable PPE protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: A70932 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Davises, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A7050; MUID:38295997; PMID:3634230 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A; Reference number: A70500; MUID:98295997; PMID:9634230 A; Accession: B70931 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-423 <col/> A; Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17722.1; IA; Experimental source: strain H37Rv	; 70, Gaps ATNLLGONTPA ATNLEGONTPA ATNIEGONTPA ATNIEGONTPA ATNIEGONTPA ATGENATOR PICASSAVAGTAA KLGGLWKTVSP FLGGAVTGP PLGGAVTGP ONGVRAMSSLG QNGVRAMSSLG	Oy 221 S	Genetics: A Genetics: A Genetics: A Genetics: B Genetics: B Genetics: B Genetics: B Genetics: B Genetics: B Genetics B Genetic

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                  A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17729.1; PID:e125461
A;Experimental source: strain H37Rv
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Collow, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Cannor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Molecule type: DNA
A;Residues: 1-413 <CD.
A;Residues: 1-413 <CD.
A;Cross-references: GB:205436; GB:AL123456; NID:g3261770; PIDN:CAB08826.1; PID:e316565;
A;Experimental source: strain H37RV
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C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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                                                                                                                                                                     92; Indels
                                                                                                                       Query Match
32.3%; Score 422; DB 2;
Best Local Similarity 42.2%; Pred. No. 1.3e-21;
Matches 108; Conservative 34; Mismatches 92
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A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17723.1; PID:e125461:
A;Experimental source: strain H37Rv
C;Genetics:
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: B70625
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, H.; Perkhill, M.; Garnier, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1989
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Nature 394, Mycobacterium tuberculosis from the complete genome A;Reference number: A0500; MUID:98295987; PMID:9634230
A;Reference number: A0500; MUID:98295987; PMID:9634230
A;Accession: B70625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 TAAVNQVSVADLISSLPNAVSGLASPVTSVLDSTGLSGIIADIDALLATPFVANIINSAV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VAWMSVTAGQAELIAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 LAWLTYTAEAAAHAGSQAMASAAAYEAAYAMTVPPEVVAANRALLAALVATNVLGINTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Gaps
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208 ----AAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASV
                                                                                      300 EGAKAAGEAAKALPAAVPAIPSAGL-SGVAGAVGQAASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
30.8%; Score 402; DB 2;
Best Local Similarity 39.6%; Pred. No. 2.9e-20;
Matches 99; Conservative 40; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AANLGRAASV 242
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Probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
S.Cole S.T.; Brosch, R.; Perkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Authors: Gares, R.; Sulston, J.E.; Paylor, K.; Whitehead, S.; Barrell, B.G.
A.Atterence number: A70500; MUID: 98295987; PMID: 9634230
A.Atterence number: A70500; MUID: 98295987; PMID: 9634230
A.Atterence number: A70500; MUID: 98295987; PMID: 9634230
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A.Atterence number: A70500; MUID: 98295987; PMID: 9848230
A.Atterence number: A70500; MUID: 98295987; PMID: 9848230
A.Atterence number: A70500; MUID: 98295987; PMID: 9848230
A.Atterence number: A70500; MUID: 98295987; PMID: 9848230
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A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17730.1; PID:e1254620
A;Experimental source: strain H37Rv
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: 17-041-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70932
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, C; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Geneles, S.; Harris, D.; Gordon, S; Connor, R.; Davies, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atile: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:964230
A;Accession: B70932
A;Accession: B70932
A;Residues; 1-468 <COL>
A;Residues: 1-468 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 NHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGV---RAMSSLGSSLGSSGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.8%; Score 389; DB 2; Length 39 37.6%; Pred. No. 2.3e-19; ive 43; Mismatches 106; Indels
231 -GVAANLGRAASVRYGHRDGGKYAXSGRRNGGPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 ASLTASLGEASSV-----GGLSVPAGWSTAAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 37.69
Matches 103; Conservative
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Best Local 9
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A, Gene: PPE
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c;Species: Mycobacterium tuberculosis
c;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: G70925
C;Accession: G70925
R;Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Raogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Tile: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70925
A;Status: preliminary, nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-408 cCOL-
A;Cross-references: GB:Z74024; GB:AL123456; NID:g3250700; PIDN:CAA98377.1; PID:e1301025; A;Genetics:
A;Genetics: PPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 SAGASQAGSVGGMSVPPSWAAATPAIRTVAAVFSSTGLQAVPAAAISEGSLLSQMALASV 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115
                                                                                                                                                                                                 72 VAWMSATAALAREAAAQASAAAAAYAATVPPPVVAANRAELAVLAATNIFGQNTGA 131
                                                                                                                                                                                                                                                                                           IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                         121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI-----SN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SMINSGVSMINILSSMLKGFAPAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LOFEASLAQQAIPGTPGGAG--DSGSSVLDSWGPTIFA-----GPR 290
                                                                                                                                                                9
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                                                                                                                                                            1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --AMSSLGSSLGSSGLGGGVAANLGRA-----ASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAA----V
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                                                                                                    Gaps
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                                                                                                    62;
                                 30.8%; Score 402; DB 2; Length 463; 35.7%; Pred. No. 3.6e-20; ive 37; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.2%; Score 395; DB 2; Length 408; 38.9%; Pred. No. 9.2e-20; Live 31; Mismatches 78; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYGHRDGGKYAXSGRRNGG 261
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Best Local Similarity 38.9%
Matches 110, Conservative
                                                                      Best Local Similarity 35.7
Matches 114; Conservative
                                                                  Similarity
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C,Accession: A70646
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Ashandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;cross-references: GB:283867; GB:AL123456; NID:G3261695; PIDN:CAB06278.1; PID:e291015; A;Experimental source: strain H37Rv
                                                                                                                                         73 VTWMSGTSAQAKAAADQARAAVVAYETAFAAVVPPPQIAANRSQLISLVATNIFGQNTAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 QLSVPPSWAAPSTRPVSALSPAGLTTLPGTDVAEHGMPGVPGVPVAAGRASGVLPRYGVR 369
                                                                                                                                                                                                                  IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEAS- 119
                                                                                                                                                                                                                                                    ------DTAAANQLMMNVPQALKQLAQPTQGTTPSSKLGGL------W 155
                                                                                                                                                                                                                                                                                                                                                                          LASGINAVITALSSAAQFPFDIIPTLLQGLA--TLSTQYTQLMGQLINAIFGPTGATTY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                156 KTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRA 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      robable PPE protein - Mycobacterium tuberculosis (strain H37RV)
;Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGGLLEQAAAVEEASD
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                                                                                                        1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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36.0%; Pred. No. 1e-18;
tive 40; Mismatches 96; Indels 56; Gaps
                                                        47; Gaps
  Length 468;
                                                     Indels
Query Match 29.6%; Score 386.5; DB 2; Best Local Similarity 37.8%; Pred. No. 4.1e-19; Matches 102; Conservative 37; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 MSSLGSSLGSSGLGGGGVAANLGRAASVRYG 245
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Best Local Similarity 36.0%
Matches 108; Conservative
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Search completed: June 30, 2004, 16:54:01

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 30, 2004, 16:42:21; Search time 4.28192 Seconds (without alignments) 3198.204 Million cell updates/sec Run on:

US-09-597-796C-26 1306 1 VAWMSVTAGQAELFAAQVRV.....YGHRDGGKYAXSGRRNGGPA 263 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q11031 mycobacteri			Q10778 mycobacteri								Q50703 mycobacteri		P35658 homo sapien	P33790 escherichia	Q10169 schizosacch	Q9fec4 chlamydomon	P47033 saccharomyc				Q8n2m8 homo sapien		P40472 saccharomyc		Q10873 mycobacteri		P14859 homo sapien	P38894 saccharomyc	Q9ul36 homo sapien	P28284 herpes simp	Q01981 emericella	11 11 2 1 m S 2 8 5 0
SUMMAKIES		XD61 MYCTU	YIO2 MYCTU	YS92 MYCTU	YF48 MYCTU	Y878 MYCTU	Y442 MYCTU	Y096_MYCTU	SRA MYCLE	YU18 MYCTU	YU21 MYCTU	YY29 MYCTU	YY25 MYCTU	BUN2_DROME	N214 HUMAN	TRG1_ECOLI		RAA3 CHLRE	PRY3 YEAST	STFR_ECOLI	FLO1 YEAST	PRY2_YEAST	SFRG_HUMAN	YM96 YEAST	SIM1_YEAST	FXC1 MOUSE	YJ83 MYCTU	CST2 HUMAN	PO21_HUMAN	FLO5_YEAST		1 1	اہا	NU62 MOUSE
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P22865 lactococcus O60269 homo sapien	P31503 rattus norv P35827 campylobact	P35828 caulobacter P51610 homo sapien	P51611 mesocricetu P27921 gallus gall	P03764 bacteriopha Q9u6al drosophila	P31368 drosophila P46839 mycobacteri
US45_LACLC Y514_HUMAN	PO21_RAT SLAP_CAMFE	SLAP_CAUCR HFC1_HUMAN	HFC1_MESAU JUND_CHICK	STF LAMBD PROS DROVI	PDM1_DROME CTPA_MYCLE
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ALIGNMENTS

us-09-597-796c-26.rsp

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Q10813;
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Geborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Squares R., Stalton S., Squares R., Bulton J.E., Mitchead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSS----LGSSLGSSGLGGGVAANL
                                                                                                                                                                                                                        VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                          Gaps
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                       5.
                                                                                                                      76.7%; Score 1001.5; DB 1; Length 396; 84.1%; Pred. No. 2.4e-62; ive 13; Mismatches 21; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                    2al protein; Complete proteome.
158 159 TA -> AT (IN REF. 2).
396 AA; 40015 MW; 6AFAE0D7B5F668D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein RV1802/MT1851/MD1830.
RV1802 OR MT1851 OR MTV049.24 OR MB1830.
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                                                                                                                 Query Match
Best Local Similarity 84.1%;
Matches 207; Conservative
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Pfam; PF00823; PPE; 1.
                    Hypothetical protein;
CONFLICT 158 159
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                                                                        SEQUENCE
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O53951;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWIL outstainnthe Bwropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 VAWMSATAALAREAAAQASAAAAAYEAAFAATVPPPVVAANRAELAVLAATNIFGONTGA
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                 MEDLINE-22709107; Pubmed:1278872;
MEDLINE-22709107; Pubmed:1278872;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Manscor H.,
Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,
Harris B., Arkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-788212003).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 463;
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Best Local Similarity 35.7%; Pred. No. 8.2e-21;
Matches 114; Conservative 37; Mismatches 106; Indels
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15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2033 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv2892c/MT2959/Mb2916c.
RV2892C OR WT2959 OR WTCY274.23C OR MB2916C.
Mycobacterium tuberculosis, and
Mycobacterium boyis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> L (IN REF. 2).
EE64828BF09FA551 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tuberculist, Rv1802, -.
InterPro, IPR000030; Microbac_PPE.
Pfam, PF00823; PPE, 1.
Hyporiterical protein; Complete proteome.
CONFLICT 401 401 S -> L (IN I
SPECIĘS=M.bovis; STRAIN=AF2122/97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 RYGHRDGGKYAXSGRRNGG 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AL022021; CAA17723.1; -- EMBL, AL00704; ARK46123.1; -- EMBL, BX248340; CAD94533.1; -- PIR; C70931; C70931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46021 MW;
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192 PPLATTAAVPQLLQQLSSTSLIPWYSALQQWLAENLLGLTPDNRMTIVRLLGISYFDEGL 251
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InterPro; IPR000030; Microbac PPE.
InterPro; IPR002899; Mycobac Dentapep.
Pfam; PF01469; Pentapeptide_2; 11.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z74020; CAA98335.1; -.
EMBL, AB007026; AAK45866.1; ALT_INIT.
PIR; A70762; A70762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                     MYCTU
                                                                                                   252
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YF48 MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                              SPECIES-M. tuberculosis, STRAIN=H37RV,
MEDLINE=9825987; PubMed=963430,
Goldon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Kroph A., Mochean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulter S., Seeger K., Skelton S., Squares R.,
Sultston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Pleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Pleischmann R.D., Wodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Mhole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=M. Dovis; STRAIN=AF2122/97;
SPECIES=M. Dovis; STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
MEDLINE=22709107; PubMed=12788972;
MEDLINE=22709107; PubMed=12788972;
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R. Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G., "The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
-! SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE007119; AAK47285.1; --
EMBL, BX248344; CAD96603.1; --
PIR, G70925; G70925.
Tuberculist; RV2892c; --
InterPro; IPR000030; Microbac_PPE.
Ffam; PF00833; PPE, Iransmembrane; Complete proteome.
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                                                                                                                                                                                                                                                                                                                           genome sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.";
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                                 SEQUENCE FROM N.A.
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          SO THE PROPERTY OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SENDENCE OF SOIL SET SO
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155 WKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holroyd S.,
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STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth I., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Osborne J., Whitchead S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G.; Pociphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.

Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.

NCBI_TaxID=1773;
                                                              291 ASPSVAGGGAVGGVQTPQPYWYWALDRESIGGSVSAALGKGSS 333
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TRANSMEM 14 34 POTENTIAL.
TRANSMEM 180 200 POTENTIAL.
                                                                                                                                                                            215 AMSSL--GSSLGS-----SGLGGGVAANLGRAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-DCT-2003 (Rel. 42, Lost annotation update)
Ryptcherical PPE-family protein Rv1548c/MT1599.
RYD1548C OR WT1599 OR MTCY48.17.
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Wed Jul

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                         123 AANQLMN--NVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANL--- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 LG-----SFNPGSANTGSVNLGNANIGDLNLGSGNIGSYNLGGGNTGDLNPDS 259
                                                                                                                                                                                                                                                                                                                      63 VNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTA 122
                                                                                                                                                                                                                                                                                                                                                                              135 AVEAVYEQMWAADVAAMLGYHGEASAVALSLTPFTPSP-----SAAATPGGAVII 184
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Biglmeder K., Gas S., Barry C.B. III, Tekkia F., Badcock K., Basham D., Brity C.B. III, Tekkia F., Davies R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Culver S., Geoger K., Schlon S., Squares R., Squares R., Stalston J.B., Taylor K., Whitehead S., Squares R., Schlon S., Squares R., Schlon S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                    3 WMSVTAGOAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGGNTPAIA
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                                                                                                                                                Gaps
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                             61;
                                                                                   19.6%; Score 255.5; DB 1; Length 678; llarity 27.3%; Pred. No. 1.7e-10; Conservative 34; Mismatches 97; Indels 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
258 258 D -> G (IN REF. 2).
678 AA; 66736 MW; 209F1593D52533A2 CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Prochetical PPB-family protein Rv0878c/MT0901.
RV0878C OR MT0901 OR MTCY31.06C.
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                                                                                                           Similarity
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                                                                                            Local Sim.
72;
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CONFLICT
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 ISWLNDATARAEGAAAAGAKAAAAVYBAARATAHPALVAANRNQLISLVLSNLFGQNLPA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 IAATEASYEQLWAQDVAAMVGYHGGASTVASQLTPWQQ------LLSVLPPVVTAAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMV---SMANNHMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61; Gaps
                                                                                                                                                                                                                                                                                          Transmembrane; Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 443;
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                                                                                                                                                                                                                                                                                                                                                                                                                        X 10 AA APPROXIMATE REPEATS.
C58BEC607F0675E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
18.6%; Score 243.5; DB 1;
Best Local Similarity 29.3%; Pred. No. 7.2e-10;
Matches 82; Conservative 38; Mismatches 99;
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                                                           entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
POLY-ALA.
                                                                                                                                                                                        Tuberculist, Rv0878c; --
InterPro; IPR000030; Microbac PPB.
InterPro; IPR002899; Mycobac Pentapep.
Pfam; PF01469; Pentapeptide_2; 4.
Pfam; PF00823; PPE; 1.
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                                                                                                                                  EMBL; AE006977; AAK45143.1; ALT_INIT. PIR; C70780; C70780.
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MEDLINE=87137260; PubMed=3029018;
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                                                                                                                  EMBL; Z73101; CAA97385.1;
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                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                               443 AA;
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                                                                                                                                                                           TIGR; MT0901;
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RA MEDILINE-82928919; PubMed-8504220;

RA GOLG S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., RA GOLG S.T., Brosch R., Barkhill J., Garnier T., Churcher C., Harris D., RA GOCOK S.V., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Davies R., Murphy J., RA Hornsby T., Jagels K., Kroph A., McLean J., Woule S., Murphy J., RA Golffers S., Seger K., Kraph A., McLean J., Woule S., Murphy J., RA Golffers S., Seger K., Kraph A., McLean J., Woule S., Murphy J., RA Golffers S., Seger K., Mitchead S., Barrell B.G., F., Murphy J., Raylor W. Mitchead S., Barrell B.G., R. Sulton J.E., Taylor K., Whitehead S., Barrell B.G., R. Sulton J.E., Taylor K., Whitehead S., Barrell B.G., R. Sulton J.E., Dolskosh, V. Belson R., Gainn M., Hatt D., Hickey E., R. Solder G. S., Geeger K., McMaham J., Khourt H., Gill J., Mikla A., R. STOLHEC FROWN N.A.

R. SIDNINE-2206494; PubMed-12218036; R. Schlor S., Eden J., Chayam L.E., Embarant J., Barrell G., Eden J., Chayam L.E., Embarant J., Chayam L.E., Embarant J., McMaham J., Khourt H., Gill J., Mikula A., RA KANDINE-2206494; PubMed-12218036; R. K. McHanda J., Khourt H., Gill J., Mikula A., RA KANDINE-2206494; PubMed-12218036; R. K. McHanda J., McHanda W., Juckey M., Jr., Venter J. C., Fraser C.M.; Mikula A., RA KANDING W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Juckey W., Ju
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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAG-----GLLEQAAA 114
                                                                                                 115 VEEASDTAAANQLMNNVPQALKQLAQPTQGTTPSSKLG------GLWKTVS---- 159
                                                                                                                                                                                   194 NTGSGNIGNNNIGNNNIGSGNTGTGNIGSGNTGSGNLGLGNLGDGNIGFGNTGSGNIGFG 253
                                                                                                                                                                                                                      ---PHRSPISNWVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAM 216
                                                                                                                                                                                                                                               254 ITGDHOMGFGGFNSGSGN-IGFGNSGTGNVGLFNS-----GSGNIGIGNS 297
 9
1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                217 SSLGSSLGSSGLGGGVAANLGRAASVRYGHRDGG-KYAXSGRRNGGPA 263
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Score 194.5; DB 1; Length 463; Pred. No. 1.8e-06;

14.9%;

Similarity

Query Match Best Local

298 GSLNSGIGTSGT---INAGLGSAGSLNTSFWNAGMQNAALGSAAGSEA 342

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MEDLINE-22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.,
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains";
"Aparenia";
                                                                                                                                                                                                                     MEDLINE=9829597; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekaia F., Badcock K., Bacham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd 'Hornsby T., Jagels K., Krogh A., McHean J., Moule S., Murphy E., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 184:5479-5490(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                            Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterinae, Mycobacteriaceae, Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z74410; CAA98932.1; -.
EMBL; AE006922; AAK44327.1; -.
EMBL; AF0056; H70750; H70750; Tuberculist; Rv0096; -.
Tuberculist; Rv0096; -.
InterPro; IPR000030; Microbac_PPE.
Fam; PF00837; PPE; I.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42D9D66A033D0DD8 CRC64;
                           01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Hypochetical PPB-family protein Rv0096/MT0105.
RV0096 OR MT0105 OR MTCY251.15.
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245
276
323
419
463 AA;
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SEQUENCE FROM N.A.
STRAIN=H37Rv;
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AL583918; CAC29919.1;
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SEQUENCE FROM N.A.
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YU18 MYCTU
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                                                                                                           61 IAVNEABYGEMWAQDAAAMFGYAAATATATILLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                         130 IALNEADYVRWWLQAADTWAAYQAVADAATVAVPSTQPAPPIRAPGG------DAAD 180
                                                                      1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA 60
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MEDLINE=3323928; PubMed=8478104;
MEDLINE=3323928; Brooks L.A., Dockrell H.M., de Smet K.A.L.,
Thompson J.K., Hussain R., Stoker N.G.;
"Sequence and immunological characterization of a serine-rich antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor W. Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutherts S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
   17; Gaps
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Rinke de Wit T.F., Clark-Curtiss J.E., Abebe F., Kolkon A.H.J.,
Jonson A.A.M., Thole J.E.R.;
"A Mycobacterium leprae-specific gene encoding an immunologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
55; Indels
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Nature 409:1007-1011(2001).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
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16-OCT-2001 (Rel. 40, Last annotation update)
Serine-rich antigen (25L) (45 kDa protein).
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                   121 T----AAANQLMNNVPQALKQLAQP 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from Mycobacterium leprae.";
Infect. Immun. 61:2145-2153(1993).
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Mol. Microbiol. 10:829-838(1993),
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53; Conservative
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Q07297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 SSSSDSLYESIDNLYDSVAQSEEHGSDSMSQSYNTCGSVAQSELCDSPFGTPSQSSQSND 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 VAWLDGNAENAGLIARVLHAVAYAFEEARAGMVPLLTVLGNIIHTMALKAINWFGQVSTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 408;
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2 X 6 AA REPEATS OF S-V-A-Q-S-E.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 AQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAAN----LGRAASV 242
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01-711-1993 (Rel. 26, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv3018c/MT3098/WT3101.
RV3018C OR MT3098/WT3101 OR MTV012.32C.
                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 191.5; DB 1;
; Pred. No. 2.6e-06;
49; Mismatches 104;
                                                                                                                                                                                                                                                       T -> S (IN REF. 2).
S -> L (IN REF. 2).
H -> D (IN REF. 2).
P -> L (IN REF. 2).
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                                                                                                                                          Antigen; Repeat; Complete proteome
                                                                  Leproma, ML0411, -.
InterPro, IPR000030, Microbac PPE.
Pfam, PF00823, PPE, 1.
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Best Local Similarity 22.

Best Tocal 70; Conservative 4
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PIR; C86960; C86960.
PIR; S33522; S33522.
PIR; S39872; S39872.
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CONFLICT
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us-09-59/-/96c-26.rsp

Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corymebacterinee, Mycobacteriaceae, Mycobacterium.

Mycobacterium tuberculosis.

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
Hypotherical PPE-family protein Rv3021c/Rv3022c/MT3106.
RV3021C/RV3022C OR MT3106 OR MTV012.35C/MTV012.36C.

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STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

A Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Gwinn M., Haft D., Hickey B., Aclonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Abelcher A., Utterback T., Waidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and Indocatory strains.";

J. Bacteriol. 184:5479-5490(2002).

M. Bacteriol. 184:5479-5490(2002).

SEQUENCE OF 160-374 FROM N.A.

STRAIN=Isolate 50410;

Patki A.H., Dale J.W.;

Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.

I. SIMILARITY: Balongs to the mycobacterial PRE family.

-! CAUTION: In strain Oshkosh the gene for this protein is interrupted in position 307 by an IS6110 element.
                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 294; 337 and 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 protein, Complete proteome. 434 AA, 43029 MW; 410673C4BD389DD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AL021287; CAA16103.1; ...
EMBL, AE007129; ARK74727.1; ALT SEQ.
EMBL, AS007129; AAK47430.1; ALT_SEQ.
EMBL, X59271; CAA41961.1; ALT_FRAME.
PIR, B70857; B70857.
TIGR, MT3088; -.
TIGR, MT31081; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuberculist, Rv3018c, --
Tuberrou, PR0010030, Microbac_PPB.
Pfam, PF00823, PPE, 1
Hypothetical_protein, Complete pro
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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                  TAAAN-----QLMMNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPH---RSPIS 166
                                                                                                                                                                                                                                                      -----MINILSSMLKGFA 197
                                                                                                                                                                                                                                                                                                                                  9
                                                                            1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                          Gaps
                                          55;
Query Match 12.1%; Score 158.5; DB 1; Length 434; Best Local Similarity 23.4%; Pred. No. 0.00053; Matches 67; Conservative 34; Mismatches 130; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                  198 PAAAAQAVO-TAAQNGVRAMSSLGSSLGS-SGLGGGVAANLGRAAS 241
                                                                                                                                                                                                                                                                                                                                                                                                        167 NMVSMANNHMSMTNSGVS-----
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RESULT 10 YU21 MYCTU ID YU21 MYCTU S: AC 053268; 053269;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EXBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/correlation and an email to license@isb-sib.ch).

CC EMBL; ALO21287; CAA16107.1; ALT_FRAME.

EMBL; ALO21287; CAA16107.1; ALT_FRAME.

DR FWBL; ALO21287; CAA16107.1; ALT_FRAME.

DR TUBErculist; Rv3021c; ...

DR TUBErculist; Rv3021c; ...

DR TUBErculist; Rv3022c; ...

DR TUBErculist; Rv3022c; ...

DR TUBErculist; Rv3022c; ...

DR TUBErculist; Rv3022c; ...

DR TUBErculist; Rv3022c; ...

DR TUBErculist; Rv3022c; ...

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DR TUBERculist; Rv3022c; ...

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DR TUBERculist; Rv3022c; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Melschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Rollonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Bishai W., Jacobs W.R. Jr., Wender J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94; Gaps
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                                                                                                                                                                                                                                                                                                   MEDLINE=5.7K;
MEDLINE=5.7K;
MEDLINE=5.2K;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
Gordon S.V., Eiglmeder K., Gas S., Bary C.E. III. Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Comnor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd &
Horneby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.",
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.1%; Score 158; DB 1; Length 435; 21.9%; Pred. No. 0.00057; vative 32; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
-!- CAUTION: Ref.1 sequence differs from that shown due frameshift in position 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 profein; Complete proteome.
299 299 G -> A (IN REF. 2).
317 320 LAGV -> VTGL (IN REF. 2).
326 326 L -> V (IN REF. 2).
435 AA, 42876 MW, 3B157643EAA8484A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
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Best Local Similarity
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Length 178;
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                             Pfam; PF00823; PPE; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 178 AA; 19811 MW; 8BE1FC025ABFBEA6 CRC64;
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Best Local Similarity 36.5%; Pred. No. 0.00054;
Matches 38; Conservative 17; Mismatches 49;
                                                                                                                                                                    11.9%; Score 156; DB 1; 37.1%; Pred. No. 0.00029; cive 16; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical PPE-family protein Rv3425. RV3425 OR MTCY78.04C.
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InterPro; IPR000030; Microbac_PPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                     Local Similarity 37.1%
tes 39; Conservative
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Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997
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16-OCT-2001
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                                                                                                    243
                                                                                                                                                                                                                                       ------WLV-----LTGMIDMFFATVGFALGVFVLVPLLEFAVVLELAILSIGW 286
                                                                                                                                                                                                                                                                                                          184 SMTNTLSS------MLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGS-SGLGGGGVAAN 235
                                                                                                                                                                                                                                                                                                                                                          93 LLPFEE-----APEMTSAGGLLEQAAAVEEASDTAAANQLMINVPQALKQLAQPTQG 144
                                                                      -ANNHMSMTNSGV
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MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Peterson J. DeBOY R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Coldon S.V., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
17-OCT-2003 (Rel. 42, Last annotation update)
18/3429 OR MT3533 OR MTCY7.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 AA.
                                                                                                                                                                    145 TTPSSKLGGLWKTVSPHRSPISNMVSM-
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Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 LGRAAS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 SGGVVS 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1773;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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3 WMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIA 62
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Coldon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holrcyd S Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Hornsby T., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Squares R., Squares R., Sulzton J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                     133. GLDAQYQQYRAQNIAVMNDYQSTARFILAYLPRWQEPPQIYGGGG 177
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SEQUENCE 176 AA; 19855 MW; B8CEF2E9463B87B0 CRC64;
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Query Match
Best Local Similarity
Matches 66; Conserv
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RA Amanatides P.G., Scherer S.E., Holt R.A., Fryns C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Holt R.A., Fryns C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Holt R.A., Fryns C.A., Henderson S.N.,

RA Amanatides P.G., Scherer S.E., Helt G., Champe M., Pfeiffer B.D.,

RA Abrill J.F., Agapatai A., An H.-U., Andrews Permach C., Baldwin D.,

Ballew R.M., Basu A., Barter E.G., Blands T.D., Bolands T.,

RA Besson K.Y., Benchan M.P., Bunler H., Goldte E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Goldte E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Goldte E., Davises P.,

RA Burtis K.C., Busam D.A., Daller H., Goldte E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davisor D., Davis S.P.,

RA Burtis K.C., Busam D.A., Daller H., Goldte E., Center A., Chandra I.,

Cherry J.M., Cawley L.E., Dahlke C., Davisor D.,

RA Burtis K.C., Busam D.A., Buller H., Goldte E., Davisor P.,

Cherry J.M., Cawley S., Dahlke C., Davis W. B.,

Cherry J.M., Cawley S., Dahlke C., Davisor P., Harris M.,

Cherry J.M., Cawley L.E., Dahlke C., Davisor P., Harris M.,

Cherry J.M., Cawley L.E., Dahlke C., Perra C., Gan P., Harris M.,

Cherry J.M., Cawley L.E., Wallen T.J., Hernandez J.R., Harris M.,

Allahim M., Kaluah F., Karper G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Allahim M., Kaluah F., Howaland T.J., Hernandez J.R., Harris M.,

Kimmel B.E., Kodira C.D., Karf C., Karitz S., Liang Y., Lin X.,

RA Harris M., Maluah F., Mayon M., Musphy L., Musphy D.M., Naplen H.,

Railon B.M., Molson K., Saunders R.D.C., Scheeler F., Shen H.,

Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Spier B., Spradiling A.C., Stapheron M., Skrong R., Sait H.,

Railos R.A., Myora B.M., Rochey M., Marshy M., Marshy D.M., Walle M. H.,

Railos R.A., Myora B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB=Eye-antennal disk;
MEDLINE=96038094; PubMed=7555710;
Treisman J.E., Lai Z.-C., Rubin G.M.;
"Shortsighted acts in the decapentaplegic pathway in Drosophila eye development and has homology to a mouse TGF-beta-responsive gene.";
Development 121:2835-2845(1995).
                                                                                                                                                                               BUNZ_DROME STANDARD; PRT; 1211 AA.
024523; 09VK78; 09VK79;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                IsoId=Q24523-2; Sequence=VSP_006670;
SIMILARITY: Belongs to the TSC-22/Dip/Bun family.
CAUTION: Ref.2 sequence differs from that shown due to erroneous
gene model prediction.
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the second optic lobe relative to the first. Plays a role in determining proper dorsal cell fates leading to the formation the dorsal appendages.

*!-*SUBCELFULAR LOCATION: Nuclear and cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
--- ALTERNATIVE SPROJUCTS:
Comment-Experimental confirmation may be lacking for some
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EMBL; AE003636; AAF53200.1; ALT_SEQ.

RENEL; AE003636; AAF53201.1; ALT_SEQ.

R PIR; T13804; T13804.

R HSSP; P80220; 1DIP.

R Flybase; FBgn0010460; bun.

R GO; GO:0007422; P:peripheral nervous system development; NAS.

R InterPro; IPR000580; TSC-22_Dip_Bun.

R ProDom; PF01166; TSC22; 1.

R ProDom; PS017189; TSC-22_Dip_Bun; 1.

R PROSITE; PS01289; TSC222; 1.

R PROSITE; PS01289; TSC222; 1.

R Transcription regulation; Nuclear protein; Alternative splicing.

T DOMAIN.
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328 MISSING (IN REF. 1).
801 801 Q -> QQQ (IN REF. 1).
1189 1195 QQVTSAA -> TS (IN REF. 2).
1211 AA; 125299 MW; 9925A9159A7051B0 CRC64;
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IsoId=Q24523-1; Sequence=Displayed;
Name=Class 1;
IsoId=Q24522-1; Sequence=External;
Name=Class 3;
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                                                                                                                                                                                                               TN----SGVSMTNTL----SSMLKGFAPAAAQAV-QTAA-----QNGV 213
                                                                          71 MWAQDAAAMFGYAAATATATLID----FEEAPEMTSAGGLLEQAAAVEEASDTAAANQL 127
                                                                                                                            ---stiadpool 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE: Implicated in a subset of acute myeloid leukemia (acute nonlymphocytic leukemia) (AML) carrying a chromosomal translocation t(6;9) (p23;q34) that results in the formation of a DEK-CAN fusion gene.

DISEASE: Involved in some cases of acute undifferentiated leukemia (AUL) through a chromosomal translocation t(6;9) (q21;q34.1) that involves NUP214/CAN and SET.

DATABASE: NAME=ALlas Genet. Cytogenet. Oncol. Haematol.;

WWW="http://www.infobiogen.fr/services/chromozancer/Genes/CAN.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - FUNCTION: May serve as a docking site in the receptor-mediated import of substrates across the nuclear pore complex.

- SUBCINIT. Homodimer. Interacts with DDX19 and NUR98.

- SUBCELLUIAR LOCATION: Nuclear pore complex. Cytoplasmic filaments.

- TISSUE SPECIFICITY: Expressed in thymus, spleen, bone marrow, kidney, brain and testis, but hardly in all other tissues or in whole embryos during development.

- DOMAIN: Contains F-G repeats.

- PTM: Probably glycosylated as it reacts with wheat germ agglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buijs A., Grosveld G.,
"The translocation (6;9), associated with a specific subtype of acute myeloid leukemia, results in the fusion of two genes, dek and can, and the expression of a chimeric, leukemia-specific dek-can mRNA."; Mol. Cell. Biol. 12:1687-1697(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Last Sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
10-Dore complex protein Nup214 (Nucleoporin Nup214) (214 kDa nucleoporin) (CAN protein).
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Kraemer D., Wozniak R.W., Blobel G., Radu A.;
"The human CAN protein, a putative oncogene product associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myeloid leukemogenesis, is a nuclear pore complex protein that the cytoplasm.", Proc. Natl. Acad. Sci. U.S.A. 91:1519-1523(1994).
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Catarrhini; Hominidae; Homo.
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MEDLINE=92195315; PubMed=1549122;
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Mammalia; Eutheria; Primates;
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CHARACTERIZATION.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1705 SSGFSSPAFGTTAPGVFGQTTFGQASVFGQSASSAASVFSFSQPGFSSVPAFGQPA-SST 1763
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EMBL outstation
                                                                                                                                                     EMBL; X64228; S26058; S26058.

PIR; S26058; S26058.

GGnew; HGNC:8064; NUP214.

MIM; 114350; -

GO; GO;0005643; C:nuclear pore; TAS.

GO; GO;000515; E:transporter activity; TAS.

InterPro; IPR004325; Nucleoporin_FG.

InterPro; IPR004325; Nucleoporin_FG.

SMART; SM00320; WD40.

Pfam; PF03093; Nucleoporin_FG; 22.

SMART; SM00320; WD40; 2.

Nuclear protein; Transport; Proto-oncogene; Chromosomal translocation;

Repeat; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 ---FEEAPEMTSAGGLLEQA----AAVEEASDTAAANQLMNNVP--QALKQLAQPTQGTT
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Enterobacteriaceae; Escherichia.
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18 X 4 AA APPROXIMATE REPEATS.
11 X 3 AA APPROXIMATE REPEATS.
PRO/SER/THR-RICH.
LEUCINE-ZIPPER 1.
LEUCINE-ZIPPER 2.
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Pred. No. 5;
and the
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the Swiss Institute of Bioinformatics
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Last annotation update)
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2090 AA;
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-!- PTM: TRAG* PROBABLY ARISES FROM THE POST-TRANSLATIONAL CLEAVAGE OF
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                                                                                                                                                                                                                                                                           STRAIN=KIZ / CR63;
Shimizu H., Saltoh Y., Suda Y., Uehara K., Sampei G., Mizobuchi K.;
Shimizu H., Saltoh Y., Suda Y., Uehara K., Sampei G., Mizobuchi K.;
"Complete nucleotide Sequence of the F plasmid: its implications for organization and diversification of plasmid genomes.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS A CRUCIAL ROLE IN DONOR-RECIPIENT CELL INTERACTIONS. REQUIRED FOR TWO STAGES OF THE CONJUGATION PROCESS:
PILUS BIOSYNTHESIS AND MATING AGGREGATE STABILIZATION. MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CAUTION: TRAG IS NOT RESPONSIBLE FOR THE N-TERMINAL ACETYLATION OF F PILIN AS STATED BY SOME AUTHORS.
                                                                                                                                             MEDLINE=94359430; PubMed=7915817; Prost L.S., Ippen-Inler K., Skurray R.A.; "Analysis of the sequence and gene products of the transfer region the F sex factor.";
                                   Firth N., Skurray R.A.; "Characterization of the F plasmid bifunctional conjugation gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
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938 TRAG* PROTEIN.

53 CYTOPLASMIC (POTENTIAL).

73 PORTEINASMIC (POTENTIAL).

329 POTENTIAL.

412 CYTOPLASMIC (POTENTIAL).

412 CYTOPLASMIC (POTENTIAL).

433 PERIPLASMIC (POTENTIAL).

938 PERIPLASMIC (POTENTIAL).

938 PERIPLASMIC (POTENTIAL).

938 PERIPLASMIC (POTENTIAL).
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BIR; S20480; S20480.
BCGGene; EG40114; traG.
Plasmid; Conjugation; Transmembrane; Inner membrane;
                                                                                       Mol. Gen. Genet. 232:145-153(1992).
STRAIN=K12;
MEDLINE=92204127; PubMed=1348105;
                                                                                                                                                                                                                       Microbiol. Rev. 58:162-210(1994).
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

:	Description	005298 mycobacteri	Q7u0e9 mycobacteri	Q7u071 mycobacteri	Q8viz3 mycobacteri	006341 mycobacteri			O53956 mycobacteri	O53950 mycobacteri		Q7tzj3 mycobacteri			O53957 mycobacteri	Q7tzh7 mycobacteri	Q99qil mycobacteri
SUMMARIES	ΔĦ	005298	Q7U0E9	Q7U071	Q8VIZ3	006341	O7TWF5	Q7TZH8	053956	053950	Q7TZI4	Q7TZJ3	053939	Q9Z5K0	053957	Q7TZH7	Q99QI1
	DB:	16	16	16	16	16	16	16	16	16	76	76	16	16	76	76	7
•	Match Length DB	391	390	396	393	393	393	399	403	423	423	393	411	421	409	409	410
* Query	Match	90.9	88.7	85.9	77.2	72.7	72.7	35.5	35.2	33.8	33.8	33.1	33.1	32.5	32.3	32.2	32.2
	Score	1187	1158.5	1122.5	1008.5	949.5	949.5	463	460	441	441	432.5	432.5	424.5	422	420	420
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Eatt D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (PPE family protein).
Mycobacterium tuberculosis.
Mycobacterium tuberculosis, Actinobacteridae; Actinomycetales; Corymebacterinae; Mycobacteridae; Actinomycetales; Corymebacterinae; Mycobacteridaeae; Mycobacterium.
NUBL TaxID=1773; laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. 391 AA PRT; PRELIMINARY; SEQUENCE FROM N.A. 005298 RESULT 1 005298

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85.9%; Score 1122.5; DB 16; Lengt
Best Local Similarity 94.3%; Pred. No. 1.1e-68;
Matches 232; Conservative 5; Mismatches 4; Indels
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MEDLINE=22709107; PubMed=12788972;
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SEQUENCE 396 AA.
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                                                                                                                                                                                                     90.9%; Score 1187; DB 16; Length 391; 99.6%; Pred. No. 4.5e-73; ive 1; Mismatches 0; Indels 0;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                         TIGR; MT1234, -..
Tuberculist; Rv1196; -..
InterPro; IR000030; Microbac_PPE.
Hypothetial protein; Complete proteome.
SEQUENCE 391 AA; 39158 MW; E409396B3ABDC0F8 CRC64;
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EMBL; Z93777; CABO: CABO: BMBL; AE007000; AAK45491.1; PIR; B70608; B70608.
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Best Local Similarity 99.6%
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SEQUENCE 390 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAVNEASYGEMWAQDAAAMFGYAAATATATEALLPFEDAPLITNPGGLLEQAVAVEEAID 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVSMASTLHSMLKGFAP-AAAQAVETAAZNGVQAMSSLGSQLGSSLGSSGLGAGVAANL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann B.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSS----LGSSLGSSGLGGGVAANL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 393;
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch P. Parkhill J., Garnier T., Churcher C., Ha Gordon S.V., Elglmeier, P., Ras S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
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Corynebacterineae; Mycobacteriaceae, Mycobacterium.
                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.2%; Score 1008.5; DB 16; Lengur
84.6%; Pred. No. 6.6e-61;
V:mmarches 19; Indels
                                                                                                                                                                                                                                                                                                                                               laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AE007161, AAK47941.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00823; PPE; 1.
PROSITE; PS00501; SPASE I 1; 1.
SEQUENCE 393 AA; 39688 MW; 86F0B67798855511 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016020; C:membrane; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GITLE-PP.O; IPR000030; Microbac PPE.
INTER-Pro; IPR000508; Peptidase S26.
Pfam; PF00823; PPE; 1.
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Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04,
01-JUN-2003 (TrEMBLrel. 24,
Hypothetical protein Rv3478,
RV3478 OR MTCY13E12.31.
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                                                Mycobacterium tuberculosis.
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les 208; Conservative
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family protein.
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                                                                                                              NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                     Bishai W.;
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Best Local &
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74 VAWMSVTAGGAQLTAAQVRVAAAAYETAYRLTVPPPVIAENRTELMTLTATNLLGQNTPA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAANQLMNNVPQALKQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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   Holroyd
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holro, Horneby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.7%; Score 949.5; DB 16; Length 393; 79.7%; Pred. No. 7e-57; ive 14; Mismatches 31; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium bovis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterinae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1765,
                                                                                                                                                                                                                                                                                                                                                                                    il protein; Complete proteome.
393 AA; 39413 MW; AF4C20C95DAE7DD4 CRC64;
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Last annotation update)
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STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
                                                                                                                                                                                                                                                                                                                         InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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                                                                                                                                                                                                      Nature 393:537-544 (1998).
EMBL: 295390; CABOR702.1; -
PIR: C70568; C70568
Tuberculist; Rv3478; -
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196; Conservative
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Matches 196; Conservative
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PPEGO OR MB3505.
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Matches 117;
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236
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                                                                                                                                                       121 TAAANQIMNNVPQALKQIAQPTQGTTPSSKLGGIWKTVSPHRSPISNMVSMANNHMSMTN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 VAWMSVTAVRAEQAGAQAGAQAEAAAAYEAAFAATVÞPÞVIEANRAQLMALIATNVLGQNAPA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 IAATEAQYAEMWSQDAMAMYGYAGASAAAT-OLTPFTEPVOTTNASGLAAQSAAIAHATG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TAAA-----GLWKTVSPALKQLAQPTQGTT---PSSKLG------GLWKTVSPH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 ASAGAQQTTLSQLIAAIPSVLQGLSSSTAATSASGPSGLLGILGSGSSWLDKLWALLDPN 251
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                                                                                          IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                                                                                                                                SGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSS----LGSSLGSSGLGGGVAANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 RSPISNMVSMANNHMSMTNSGVSM-TNTLS---SMLKGFAPAAAAQAVQTAAQNGVRAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJINE-22709107; PubMed=12788972; Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Dogett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; Embl.; BX248340; CAD94539.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.5%; Score 463; DB 16; Length 399; 43.7%; Pred. No. 1e-23; ative 36; Mismatches 72; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 AA; 38840 MW; 1A0F4377318E74F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 GLGGALVAPLGSAGGLGGTVAAGLGNAATV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 43.7%
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  PPE family protein.
PPE31 OR MB1836.
                                                                                                                                                                                                                                                                                                                                    GRAASV 242
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SEQUENCE 399 AA;
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RESULT

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217
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SPRAINH137KV.

BOTALINH137KV.

MEDLINE=98295987; PubWed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

Cole S.T., Elgianeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Badcock K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Nurphy L.,

Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Bulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 ASAGAQQTTLSQLIAAIPSVLQGLSSSTAATFASGPSGLLGIVGSGSSWLDKLWALLDPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Belchier A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                           Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.2%; Score 460; DB 16; Length 403; 43.3%; Pred. No. 1.7e-23;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17728.1;
EMBL; AE007044; AAK46128.1;
PIR; H70931; H70931
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238 238 V -> L (IN REF. 2).
403 AA; 39243 MW; DCE18880FD15CBFE CRC64;
                                                            (TremBlrel. 06, Created)
(TremBlrel. 06, Last sequence update)
(TremBlrel. 24, Last annotation update)
403 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GLGGALVAPLGSAGGLGGTVAAGLGNAATV 330
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36; Mismatches
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Tuberculist; Rv1807; -.
Interbro; IPR000030; Microbac_PPE.
Pfam; PP00823; PPE; 1.
                                                                                                                                                               PPE-family protein. RV1807 OR MT1856 OR MTV049.29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 393:537-544 (1998).
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PRELIMINARY;
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61 IAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 HRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 YTFP-----GVLPPSGVPYLLGIQSVL-------VTQNGQGVSALLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAN-----SSKIGGLWKTVSP
                                                                                                                                                                                                                                                                                               MEDINE-22709107; PubMed=12788972; Medina N., Mansoor H., MEDINE-2709107; PubMed=12788972; Medina N., Mansoor H., Paron E., Eiglmeier K., Camus J.-C., Medina N., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Doggett J., Gordon S.V., Hewinson R.G.; Parkhill D.G., Colle S.T., Gordon S.V., Hewinson R.G.; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.8%; Score 441; DB 16; Length 423; 41.2%; Pred. No. 3.5e-22; ive 30; Mismatches 67; Indels 70
                                                                                                                                                                                                 Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SLGSSGLGGG-VAANLGRAASV 242
284 KIGGKPITGALAPLAEFALHTPILGSEGLGGGSVSAGIGRAGLV 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 AA; 41477 MW; 26E52CC271FBBF57 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 117; Conservative
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                                                                                 PRELIMINARY;
                                                                                                                               1-OCT-2003 (TrEMBLrel.
1-OCT-2003 (TrEMBLrel.
                                                                                                               (TrEMBLrel.
                                                                                                                                                                   PPE family protein.
PPE29 OR MB1829.
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PPE26 OR MB1817.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 423 AA;
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                                                                                                                                                                                                                                                  NCBI_TaxID=1765;
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                                                                                                                 01-OCT-2003
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                                                                                                                               01-OCT-2003
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                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                 Q7TZI4
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                                        RESULT
                                                                 Q7TZI4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAAAN-----SLMMNVPQALKQLAQPT----QGTTP-----SSKLGGLWKTVSP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GVLPPSGVPYLLGIQSVL-------VTQNGQGVSALLG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VAWMSVTAGOAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAAGGNLQSAFPQLLSAVPRALQGLALPTASQSASATPQWVTDLGNLSTFLGG--AVTGP
                                                                                                                                                                                                                                                                                                             Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R. Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Squares R., Schelton S., Squares R., Felton J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.8%; Score 441; DB 16; Length 423; 41.2%; Pred. No. 3.5e-22; tive 30; Mismatches 67; Indels 70
                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SLGSSGLGGG-VAANLGRAASV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17722.1; -.
EMBL; AE007044; AAK46122.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 AA; 41477 MW; 26E52CC271FBBF57 CRC64;
                                                                                                               Last sequence update)
Last annotation update)
                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculist; Rv1801; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                  MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                 RV1801 OR MTV049.23 OR MT1850.
                                                                                            01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                               PRELIMINARY;
                                                                                                                                                 PPE-family protein.
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les 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE 423 AA
                                                                                                                                                                                                                                  NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; MT1850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                    STRAIN=H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bishai W.;
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131 120

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Score 424.5;
EMBL; AL022021; CAA17711.1; ALT_INIT.
EMBL; AE007043; AAK46108.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 MLG----GGPVAAGLGNAASV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=TN;
MEDLINE=21128732; PubMed=11234002;
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                                                                    TIGR; MT1838; --...
Luberculist; Rv1789; -..
LuterPro; LR000030; Microbac_PPB.
Pfam; PF00823; PPB; 1.
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                                                                                                                                                                                                                               Query Match
Best Local Similarity 41.0%
Matches 107; Conservative
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                                            PIR; G70929; G70929.
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                                                                                                                                                                  Complete proteome. SEQUENCE 411 AA;
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SEQUENCE: 421 AA
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Barrell B.G.;
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Q9Z5K0
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                                                                                                                                                                                                                                                                                                                                                                                                                            250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 ASFEYNTEGIPYFSIGMGNNFIQAAKTL-GLIGSAAPAAVA----AAGDAAKGLPGLGGG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TAAA--NQLMNNVPQALKQLAQPTQGTTPSSKLGGLWK------TVSPH 161
                                                                                                                                                                                                                                                                                                         1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGS
  Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Kealing L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete gen
                                                                                                                                                                                                                                                            31; Gaps
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Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey B.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-9825987; PubMed-9634230; Cole S.T., Encore C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III. Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Davin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulton J.E., Taylor K., Whitehead S., Barrell B.G.; Poology of Mycobacterium tuberculosis from the Complete genome sequence.";
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                                                                                                                                                                                                           Match 33.1%; Score 432.5; DB 16; Length 393; Local Similarity 41.0%; Pred. No. 1.2e-21; es 107; Conservative 38; Mismatches 85; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPE-family protein.
RV1789 OR MT1838 OR MTV049.11.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
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Paboratory strains.";
Submitted (APR-2018) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  393 AA; 38572 MW; 41944B6E547A8AB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 MLG----GGPVAAGLGNAASV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 SLGSSGLGGGVAANLGRAASV
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Matches
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053939
         SARTARA
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61 IAVNEABYGEMWAQDAAAMFGYAAATATATLLPFEBAPEMTSAGGLLEQAAAVEEASD 120
                                                                                                                                                                                                                                                                                                                                                   269 ASFFYNTEGLPYFSIGMGNNFIQSAKTL-GLIGSAAPAAVA----AAGDAAKGLPGLGG 322
                                                                                                                                                                                                                                              91 VAWMSAAAAQAEQAATQARAAAAAAFBAAFAATVPPPLIAANRASLMQLISTNVFGONTSA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                           161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 TAQSTLTEMITGLPNALQSLTSPLLQSS-NGPLSWLWQILFGTPNFPTSISALLTDLQPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wheeler P.R. Honore N. Garnier T. Churcher C. Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Basham D., Brown D., Chillingworth T., Connor R.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Marlean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Saguares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                  1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
                                                                                                                            31; Gaps
                                                               DB 16; Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43119 MW; 680FDSFDCB65B4A7 CRC64;
411 AA; 40557 MW; 03C90B5E0590B7DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TAAA--NQLMNNVPQALKQLAQPTQGTTPSSKLGGLWK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0925K0 PRELIMINARY; PRT; 421 AA. 0925K0 925K0; 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-UM-2003 (TrEMBLrel. 24, Last annotation update) Putative PPE procedin (PPE-family protein). MI1182 OR MLCB1701.08C.
                                                         33.1%; Score 432.5; DB 16;
41.0%; Pred. No. 1.3e-21;
tive 38; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL049191; CAB39148.1; -.
EMBL; AL583921; CAC31563.1; -.
Leproma; ML1182; -.
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DB 16; Length 421;

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32.3%; Score 422; DB 16;
42.2%; Pred. No. 6.6e-21;
ive 34; Mismatches 92
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MEDLINE=22709107; PubMed=12788972;
                                                                                                                                                                                                                                                                                                                                                                                                                                       227 GLGGGVAANLGRAASV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 PLGGGATGGIARAIYV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 25, C
(TrEMBLrel. 25, I
(TrEMBLrel. 25, I
                                           Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPE family protein.
PPE32 OR MB1837.
                         Similarity
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SEQUENCE 409 AA;
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O7TZH7;
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A.,
Fleischmann T., Hackey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.,
"Whole genome comparison of Mycobacterium tuberculosis clinical and
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                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
; Pred. No. 4.6e-21;
36; Mismatches 99; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17729.1; -.
EMBL; AZ007044; AZK46129.1; ALT_INIT.
PIR; A70922; A70932.
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SEQUENCE 409 AA; 39917 MW; 1E15202BACF36379 CRC64;
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InterPro, IPR000030; Microbac_PPE
Pfam; PF00823; PPE; 1.
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                       Matches 104; Conservative
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  Similarity
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                                                                                                                                                                                                                                                                                                                                                          174 NHMSMINSGVS-----MINILSSMLKGFAPAAAAAAVOIAAONGVRAMSSL-GSSLGS-S
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                                                                                                     1 VAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPA
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                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1765;
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DB 16;
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Search completed: June 30, 2004, 16:52:53 Job time: 20.156 secs

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June 30, 2004, 16:44:57; Search time 22.1761 Seconds (without alignments) 1697.113 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES

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-950-60	US-09-072-596-80	-072-	US-09-073-009-126	US-09-073-010-126	US-09-287-849-28	US-09-620-412C-341	US-09-598-419-341	US-09-620-412C-333	US-09-598-419-333	US-09-620-412C-321	US-09-598-419-321	US-09-620-412C-329	US-09-598-419-329	US-09-620-412C-325	US-09-598-419-325	US-09-556-877-196	US-09-620-412C-196
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RESULT 140-2 Sequence 2, Application US/09223040 Sequence 2, Application US/09223040 Sequence 2, Application US/09223040 Sequence 2, Application US/09223040 Sequence 2, Application Sequence 3, Application APPLICANT: Skeiky, Yasir APPLICANT: Gampos-Neto, Antonio APPLICANT: Campos-Neto, Antonio APPLICANT: Coriac Corporation TITLE OF INVENTION: Toxion Proteins of Mycobacterium tuberculosis Antigens TITLE OF INVENTION: and Their Uses TITLE OF INVENTION: and Their Uses FILE REFERENCE: 014058-00901008 CURRENT PAPLICATION NUMBER: US/09/223,040 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 2 LENGTH: 729 LENGTH: 729 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-223-040-2	Query Match Best Local Similarity 100.0%; Pred. No. 3.6e-261; Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 MEHHHHHTAASDNFOLSOGGGGFALPIGGAWAIAGOIRSGGGSPTVHIGPTAFLGLGVVD 60	61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAWADALNGHHPGDVISVTWQ 120	121 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL 180 	181 FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVARMSVTAGQAELTAAQVRVAAAAYE 240 	241 TAYGLTVPPPVIAENRAELMILIATNILGGNTPAIAVNBABYGEMWAQDAAAMFGYAAAT 300 241 TAYGLTVPPPVIAENRAELMILIATNILGGNTPAIAVNBABYGEMWAQDAAAMFGYAAAT 300	301 ATATATLLPPEBAPEMTSAGGLLEQAAAVEBASDTAAANQLMNNVPQALQQLAQPTGGTT 360
RESULT 1 US-09-233-04(US-09-233-04(Sequence 2) Patent No. GENERAL INO. APPLICANT APP	Query Ma Best Loc Matches	දු දු	\ 6	S S	දු දු	\ \ \ \ \	δλ

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APPLICANT: Reed, Steven G.
APPLICANT: Reekly, Yasir A.W.
APPLICANT: Dillon. Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens FILE REFERENCE: 014058-009020US
CURRENT APPLICANTON NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
                                                                          61_NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ
                                                                                                                                                                      121 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
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    WHHHHHHAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
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UMBER: US 08/942,578
1997-10-01
UMBER: US 09/025,197
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APPLICANT: Action Covin C.
APPLICANT: Allow Davin C.
APPLICANT: Allow Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Allow Davin C.
APPLICANT: Campos-Netc, Artconio
APPLICANT: Campos-Netc, Artconio
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APPLICANT: Campos-Netc, Artconio
APPLICANT: Campos-Netc, Artconio
APPLICANTON: Braion Protiens of Mycobacterium tuberculosis Antigens
FILES REFERENCE: 014058-009020US
FILES REFERENCE: 014058-009020US
FILES REFERENCE: 014058-009020US
FILES REFERENCE: 1099-04-07
FRIOR APPLICATION NUMBER: US 08/42,578
FRIOR FILING DATE: 1997-03-13
FRIOR PILING DATE: 1998-04-07
FRIOR PELING DATE: 1998-04-07
FRIOR APPLICATION NUMBER: US 09/025,197
FRIOR APPLICATION NUMBER: US 09/025,197
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FRIOR APPLICATION NUMBER: US 09/025,197
FRIOR APPLICATION NUMBER: US 09/025,197
FRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN VET: 2.1
LENGTH: 729
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-2
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
FILE REFERENCE: 014058-009020US
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; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
US-09-287-849-26
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PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SSQ ID NO 26
LENGTH: 596
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US-09-287-849-22
Sequence 22, Application US/09287849
Patent No. 6627198
GENERAL INFORMATION:
                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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53.4%; Score 1967.5; DB 4; Length
Best Local Similarity 72.0%; Pred. No. 1e-135;
Matches 431; Conservative 19; Mismatches 82; Indels
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-00-01
PRIOR FILING DATE: 1997-00-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SECTWARE: PALENTIN VOY: 2.1
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ORGANISM: Artificial Sequence
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                      APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Attonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Variazik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: WARDERS: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUMLARI CONTROLL SHOWN TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE TO SEE 
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CLASSIFCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPRONE: (206) 622-4900
TELEPRONE: (206) 622-4900
TELEPRONE: (206) 622-4900
TELEPRONE: (206) 622-4900
SEQUENCE CHARACTERISTICS:
                                                                                  Sequence 102, Application US/08818111
Patent No. 6338852
                                                                                                                                                                                                                        Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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Best Local Similarity 99.7
Matches 390; Conservative
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                                                                                                                                                                              GENERAL INFORMATION:
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US-08-818-111-102
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Daniel R.
APPLICANT: Vedvick, Daniel R.
APPLICANT: Vedvick, Daniel R.
APPLICANT: Vedvick, Daniel R.
APPLICANT: Vedvick, Indenovation Result of Tuber OF Invention Result of Tuber OF Invention Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of Tuber Result of
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Pred. No. 3e-134;
0; Mismatches 1; Indels
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APPLICATION NUMBER: US/08/818,112 FILING DATE: 13-MAR-1997 CLASSIPICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
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ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPRA: (206) 682-6031
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.7%;
Matches 390; Conservative
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TYPE: amino acid
STRANDEDNESS: single
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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APPLICANT: Campoe-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardaik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1944; DB 4; Length 3:
Pred. No. 3e-134;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
               502 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
                                                                                                                                                                                  Sequence 102, Application US/09072596; Patent No. 6458366
GENERAL INFORMATION: APPLICANT: Reed, Steven G. APPLICANT: Reed, Steven G. APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 21012
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
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99.7%;
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Best Local Similarity
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STREET: 6300 CO
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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US-09-072-596-102
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                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.7%; Score 1944; DB 4; Length 391; 99.7%; Pred. No. 3e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEPY disk
COMPUTER: BEADABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                            361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                Sequence 107, Application US/09056556
Patent No. 6350456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 99.7
Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-09-056-556-107
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                                                                                                                                                US-09-056-556-107
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121 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 180
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                                                                                                                                                181 ILEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 240
                                                                                                                                                                                                                                                 241 MYSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
                                                                                                                                                                                                                                                                                                                                  262 LIATNIJGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG 321
                                                                                                   LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381
                                                                                                                                                                                                                                                                                                   442 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 501
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Wedvick, Daniel R.
APPLICANT: TWENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER.OF SQUENCES: 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: SEED and BERRY LLP (6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
44.8%; Score 1652.5; DB 3;
Best Local Similarity 84.9%; Pred. No. 6.2e-113;
Matches 337; Conservative 19; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                 502 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                              361 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 111, Application US/08818112
Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INPOMENTION:
NAME: MAKL, DAVIG J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE. CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
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CITY: Seattle
STATE: Washingt
COUNTRY: USA
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US-08-818-112-111
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301 LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 360
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MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQTAAQNGVRAMSSLGSSLGSSG 441
                                            241 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG 300
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                                                                                           442 IGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIG
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APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.7%; Score 1944; DB 4; Length 391; Best Local Similarity 99.7%; Pred. No. 3e-134; Matches 390; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: 05-WAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                             502 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
                                                                                                                                                                                                                         361 GQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Maki, David J
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Paliti
                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 107, Application US/09072967
; Patent No. 6592877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed, Steven G.
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linear
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STREET: 6500
CITY: Seattle
STATE: Washington
USA
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reed,
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US-09-072-967-107
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US-09-072-967-107
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
Best Local Similarity 84.9
Matches 337; Conservative
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                                                                                                                            300 GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
                                                              MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQTAAQNGVRAMSS----LGSSL 437
                                                                                                                                                                                                                                                                438 GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGOMLG 497
                                                                                                        LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGG 321
                                                                                                                                                                          LLEQAAAVEEASDTAAANQLAMAVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381
                                      SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261
   VVDFGALPPEINSARMYAGPGSASLVAAAKWWDSVASDLFSAASAFQSVVWGLTTGSWIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghten, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twandzik, Daniel R.
ITILE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR.1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                     498 GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 532
                                                                                                                                                                                                                                                                                                                                                                                                                        360 GLPLGOLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: MAKT, DAVID 43
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-6900
TELEPAK: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 106, Application US/08818111
Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and 1
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US-08-818-111-106
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Length 396;

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44.8%; Score 1652.5;

Query Match

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                                                                                                                                                                                                                                                                                                                                                           LIEGAAAVEEASDTAAANQIMNNVPQALQQLAQPTQGTTPSSKLGGIWKTVSPHRSPISN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGFGQMLG 497
                                                                142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 201
                                                                                                                                                                                                                61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                          LIAINLLGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTAAQNGVRAMSS----LGSSL
                                                                                                                                                                  202 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                    Gaps
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                    7;
84.9%; Pred. No. 6.2e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN P. Compatible
COMPUTER: Patent: PC-DOS/MS-DOS
SOFTWARE: Patent: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/05/056,556
FLING DATE: 07-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498 GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 GLPLGÓLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 111, Application US/09056556; Batent No. 6350456; GENERL INFORMATION: APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUNDS AND MET NUMBER OF SEQUENCES: 241 CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES: SEED and BERRY Lip STREET: 6300 Columbia Center, 701 F CONTY: Seattle STATE: Washington COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MAKL, DAU1d J.
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 2101
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-6031
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142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 201
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                                                                                                                                                                                                 34; Indels
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                                                                                                                                                   44.8%; Score 1652.5; DB 4; 84.9%; Pred. No. 6.2e-113; ive 19; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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CORRESPONDENCE ADDRESS: ADDRESSEE: SEED and BERRY LLP
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
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AND DIAGNOSIS
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Patent No. 6592877
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Dillon, Davin C.
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APPLICANT: Reed, Steven G.
SEQUENÇE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE; amino acid
                                                                                                                                                                                              Matches 337; Conservative
                                                                                          linear
                                                                                                                                                   Query Match
Best Local Similarity
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                                             TYPE: amino STRANDEDNESS
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US-09-072-967-111
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                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                               382 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTAAQNGVRAMSS----LGSSL 437
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                                                                                                                               9
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                                                                                                               142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                     202 SSAGIMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                   LIATNLLGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                                     121 LIATNILGÓNTPAIAVNEAEYGEMMAQDAAMFGYAATAATATEALLPFEDAPLITNPGG
                                               Gaps
                                        7;
    Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Skeiv, Yasir A.W.
APPLICANT: Skeiv, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
WUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                           34; Indels
  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLPVGQMGARAG - GGLSGVLRVPPRPYVMPHSPAAG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADUKESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
44.8%; Score 1652.5; DB 4; 84.9%; Pred. No. 6.2e-113; ive 19; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DEVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 106, Application US/09072596
Patent No. 6498366
GENERL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 106:
                    Best Local Similarity 84.9%
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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Query Match
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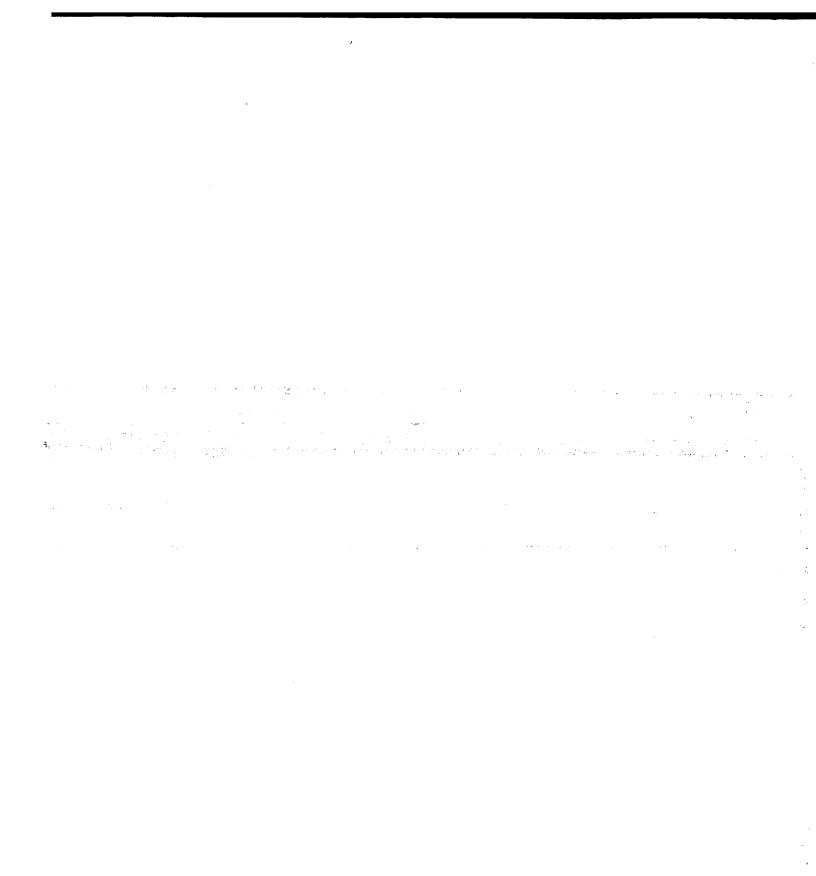
us-09-597-796c-12.rai

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Search completed: June 30, 2004, 16:55:22
Job time: 24.1761 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 359 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS:
1 TOPOLOGY: linear
US-08-818-112-109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.8%; Score 1652.5; DB 4; Length 396; 84.9%; Pred. No. 6.2e-113; ive 19; Mismatches 34; Indels 7;
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 532
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6300 Columbia Center, 701 Fifth Avenue
ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TERE: amino acid
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US-08-818-112-109
; Sequence 109, Application US/08818112
; Patent No. 6290969
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 84.9
Matches 337; Conservative
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STREET: 6300 CC
CITY: Seattle
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61 SSAGLMAAAASPYVAWMSVTAGQAQLTAAQVRVAAAAYETAYRLTVPPPVIAENRTELMT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQTAAQNGVRAMSS----LGSSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
40.3%; Score 1486.5; DB 3; Length
Best Local Similarity 84.2%; Pred. No. 7.3e-101;
Matches 303; Conservative 16; Mismatches 36; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTONNY/AGRAT INPORMATION:
NAME: MAKI, DAVIG J. 1392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPRAK: (206) 622-4900
TELEPRAK: (206) 622-4900
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
```



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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 30, 2004, 16:52:58; Search time 56.8458 Seconds (without alignments) 3625.462 Million cell updates/sec Run on:

1 MHHHHHHTAASDNFQLSQGG......SGGPVVNGLGQVVGMNTAAS 729 US-09-597-796C-12 3686 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: 1166195 seqs, 282705291 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PUSNB VUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PUSNB VUB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	Sequence 16, Appl	Sequence 2, Appli	Sequence 16, Appl	Sequence 2, Appli	Sequence 21, Appl	Sequence 15, Appl	Sequence 14, Appl	Sequence 13, Appl	Sequence 65, Appl	Sequence 12, Appl	Sequence 18, Appl	Sequence 17, Appl	Sequence 16, Appl	Sequence 18, Appl
	ΠD	US-09-287-849-2	US-09-886-349A-16	US-10-359-460-2	US-10-098-732A-16	US-10-359-459-2	US-10-369-983-21	US-10-369-983-15	US-10-369-983-14	US-10-369-983-13	US-10-098-732A-65	US-10-369-983-12	US-10-369-983-18	US-10-369-983-17	US-10-369-983-16	US-09-886-349A-18
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do	Query Match	100.0	100.0	100.0	100.0	100.0	99.8	99.8	99.8	99.8	99.8	99.8	99.8	99.8	8.66	8.66
	Score	3686	3686	3686	3686	3686	3680	3680	3680	3680	3680	3680	3680	3680	3680	3677
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US-10-098-732A-18	0-369	-287-849-2	9-886-349A-	0-359-460-	-10-098-73	0-369	883-	849-	3-10-359-460-	US-09-886-349A-14	10-193-002-1	ч	LO-098-732A	US-09-872-186-8	-002	-843-11	-122A-624	4-6489	-002-10	0-084-843-10	-287-849-	-10-359	9-886-349A-	0 - 193 - 002 - 9	-843-	S-10-098-732A-	09-712-363-16	3-09-886-34	US-10-098-732A-4
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8.66	8.66	79.8	79.8	79.8	79.8	71.5	71.4	53.4	53.4	52.7	52.7	52.7	52.7	52.3	44.8	44.8	42.9	42.9	40.3	40.3	32.1	32.1	32.1	32.1	32.1	32.1	26.8	26.8	26.8
3677	3677	2941	2941	2941	2941	2637	2631	1967.5	1967.5	1944	1944	1944	1944	1929	1652.5	1652.5	1583	1583	1486.5	1486.5	1184	1184	1182	1182	1182	1182	686	987	987
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
APPLICANT: Read, Seven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Billon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
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APPLICANTON: and Their Uses
FILE REPERENCE: 014058-00920US
FURBENT PILING DATE: 1999-04-07
PRIOR PRILING DATE: 1997-03-18
PRIOR PELLING DATE: 1999-04-07
PRIOR PELLING DATE: 1998-04-07
PRIOR PELLING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/026,556
PRIOR PELLING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR PELLING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
US-09-287-849-2
US-09-287-849-2; Sequence 2, Application US/09287849; Patent No. US2002009459A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Length 729;

Score 3686; DB 9; Pred. No. 7.5e-244;

100.0%; 100.0%;

Query Match Best Local Similarity

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RESULT 3
US-10-359-460-2
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                                       NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ
                                                                                                                                                                                            FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE
                                                                                                                                                                                                                                           TAYGLTVPPPVIAENRAELMILIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAAT
                                                                                                                                                                                                                                                                                             ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT
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                                                                         NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ
                                                                                                                          TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
                                                                                                                                         TKSGGTRTGNVTLAEGPPAEFWVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
                                                                                                                                                                           FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE
                                                                                                                                                                                                                                                                            ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT
                                                                                                                                                                                                                                                                                                                             PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQ
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  Gaps
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US-09-866-349A-16
Sequence 16, Application US/0986349A
Publication No. US20040086523AI
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-20
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OTHER INFORMATION: Description of Artificial Sequence:tri-fusion

OTHER INFORMATION: protein MTB72F (Ral2-TbH9-Ra35 or MTB32-MTB39

OTHER INFORMATION: fusion)

US-09-886-349A-16
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; Publication No. US20030147911A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  100.0%;
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO-16
LENGTH: 729
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 729, Conservative
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APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Autigen
TITLE OF INVENTION: Leishmania Autigen
FILE REFERENCE: 014058-012010018;
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Description of Artificial Sequence:tri-fusion ) OTHER INFORMATION: protein MTB72F (Ral2-TbH9-Ra35 or MTB32-MTB39; CTHER INFORMATION: fusion) 05-10-098-732A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 16, Application US/10098732A; Publication No. US20030175294A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                 VVGMNTAAS 729
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                                            APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE CR INVENTION: Tand Their Uses
TITLE OF INVENTION: Tand Their Uses
TITLE CR INVENTION: Tand Their Uses
FILE REFERENCE: 014058-0030-003
CURRENT PILING DATE: 2003-02-05
FRIOR APPLICATION NUMBER: US 08/918,112
PRIOR APPLICATION NUMBER: US 08/918,112
PRIOR APPLICATION NUMBER: US 08/918,112
PRIOR PILING DATE: 1997-03-13
FRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR PELING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-06
PRIOR FILING DATE: 1998-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
Red, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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                                                              TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAMFGYAAAT
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APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Corporation
TITLE REPERBENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369, 983
CURRENT FILING DATE: 2003-02-18
PRIOR FILING DATE: 2003-02-18
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22-15
SOFTWARE: Patentin Ver. 2.1
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US-10-369-983-21
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LENGTH: 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Skeiky, Yasir
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: Rusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REPERENCE: 014058-009010US
CURRENT APPLICATION NUMBER: US/09/10/359,459
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/223,040
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN UPF: 2.1
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                         PSSKLGGLWKTVSPHRSPISNWVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQ
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Publication No. US20040013677A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: Guderian, Jeff
APPLICANT: Codesian, Jeff
APPLICANT: Corixa Corporation
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APPLICANT: Corixa Corporation
FILE REFERENCE: 014058-009081US
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
PRICE APPLICATION NUMBER: US 60/357,351
PRICE APPLICATION DATE: 2002-02-18
                   Length
                                                  Indels
                Score 3680; DB 15;
Pred. No. 2.2e-243;
0; Mismatches 1;
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                   99.8%;
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Best Local Similarity 99.9
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TYPE: PRT ORGANISM: Artificial Sequence ORGANISM: Artificial Sequence: FEATURE: OTHER INFORMATION: Description of Artificial Sequence: fusion protein OTHER INFORMATION: MTBBIF (MTB72F-DPV)
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Publication No. US2003023559341
GENERAL INFORMATION
APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis FILE REPERENCE: 014058-0009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
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PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 813
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                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence:fusion protein; OTHER INFORMATION: MTB83F (MTB72F-MTI)
US-10-369-983-14
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                                                                                                                                                                      Indels
                                                                                                                                             Score 3680; DB 15;
Pred. No. 2.3e-243;
0; Mismatches 1;
                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                             Query Match
Best Local Similarity 99.9%;
Matches 728; Conservative
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 825
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Sequence 13, Application US/10369983 Publication No. US20030235593A1 GENERAL INFORMATION:

US-10-369-983-13

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APPLICANT: Skeiky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Redd, Steven
APPLICANT: Redd, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US 60/359, 983
CURRENT FILING DATE: 2003-02-18
FRIOR APPLICATION NUMBER: US 60/357, 351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                           LENGTH: 875
TYPE: PRT
ORGANISM: Artificial Seguence
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US-10-369-983-13
                                                                                                                                                                                                                                                                           SEQ ID NO 13
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US-10-369-983-12
; Sequence 12, Application US/10369983
; Publication No. US2030235593A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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COTHER INFORMATION:
US-10-369-983-12
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OTHER INFORMATION: (195f) fusion construct, TB MTB72F (Ral2-TDH9-Ra35)
OTHER INFORMATION: linked to Leishmania thiol-specific antioxidant
OTHER INFORMATION: (TSA or MAPS)
US-10-098-732A-65
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llarity 99.9%; Pred. No. 2.6e-243;
Conservative 0; Mismatches 1;
                                                                         RESULT 10
US-10-098-732A-65

Sequence 65, Application US/10098732A
PULICATION NO. US20330175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Groixa Corporation
TITLE OF INVENTION: Leishmania Antigen
FILE REFRENCES: 010458-012010US
CURRENT PAPLICATION NUMBER: US/10/098,732A
CURRENT FILING DAIE: 2003-04-29
PRIOR APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DAIE: 2001-03-13
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DAIE: 2001-03-13
SOFFWARE: PATENTIN VOICE: 201-03-13
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
729
                              VVGMNTAAS 729
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VVGMNTAAS
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Best Local Simi
Matches 728;
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APPLICANT: Skeiky. Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Greed, Steven
TILLONI: Corisa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2002-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR PLILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
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99.9%; Pred. No. 2.6e-243;
iive 0; Mismatches 1;
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APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Goderian, Jeff
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
CURRENT FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369, 983
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR PILING DATE: 2002-02-15
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llarity 99.9%; Pred. No. 3e-243;
Conservative 0; Mismatches 1; Indels 0;
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1
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LENGTH: 1022
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Fublication No. US20030235593A1
Fublication No. US20030235593A1
Fublication No. US20030235593A1
FUBLICANT: Guderian, Jeff
APPLICANT: Groor Seven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US5078710369,983
CURRENT FILING DATE: 2003-02-18
FRIOR PAPLICATION NUMBER: US 60/357,351
FRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
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CTHER INFORMATION: Description of Artificial Sequence:fusion protein
CTHER INFORMATION: WTB103F (WTB72F-85b)
US-10-369-983-18
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TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-369-983-16
is Sequence 16, Application US/10369983
is Publication No. US20030235593A1
is GENERAL INFORMATION:
is APPLICANT: Skeiky, Yasir
is APPLICANT: Reed, Steven
is APPLICANT: Reed, Steven
is APPLICANT: Reign Proteins of Mycobacterium Tuberculosis
if TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
if FILE REPERBNCE: 014058-09081US
if CURRENT FILING DATE: 2003-02-18
is PRIOR FILING DATE: 2003-02-15
is NUMBER OF SEQ ID NOS: 22
is SOFTWARE: Patentin Ver. 2.1
is SEQ ID NO 16
in LENGTH: 1154
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US-10-369-983-16
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ORGANISM: Artificial Sequence
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Publication No. US20040086523A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/897,796
PRIOR FILING DATE: 2000-06-20
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Length 1154;
                                            Indels
Query Match 99.8%; Score 3680; DB 15;
Best Local Similarity 99.9%; Pred. No. 3.5e-243;
Matches 728; Conservative 0; Mismatches 1;
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PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
ORGANISM: OTHER INFORMATION: Description of Artificial Sequence:MTB72FMutSA
OTHER INFORMATION: (Ra12-TbHp-Ra35MutSA)
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Search completed: June 30, 2004, 17:14:48 Job time : 58.8458 secs

5.1.6	Compugen Ltd.
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	(c) 1993
	Copyright

OM protein - protein search, using sw model

June 30, 2004, 16:43:31; Search time 19.0527 Seconds (without alignments) 3680.509 Million cell updates/sec US-09-597-796C-12 3686 1 MHHHHHHTAASDNFQLSQGG.....SGGPVVNGLGQVVGMNTAAS 729

Run on:

Title: Perfect score: 3 Sequence: 1

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

283366 segs, 96191526 residues

Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		PPE prot	PPE	•~	cal pro	PPE	secr	probable PPE prote	PPE	y pr	PPE	PPE	PPE	PPE	probable PPE prote	PPE	PPE	PPE		PPE	PPE	PPE	probable PPE prote	PPE	PPE	PPE	PPE	PPE	PPE
EDS.	B70608	2	C70568	\circ	S47170	0	\sim	A70932	O	H87056	H70931	0	F70560	0	\circ	C70931		G70881		H70929	E70929	A70882	C70582	9	S	067	A70663	7057	7096
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Result No.		N	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59

442 IGGGVAANIGRAASVGSLSVPQAWAAANQAVTPAARALPLITSLITSAAERGPGQMLGGLPV 501

\$ a \$

502 GQMGARAGGGLSGVLRVPPRPXVMPHSPAAG 532

probable PPE prote	probable PPE prote	probable PPE prote		probable PPE prote			probable PPE prote	probable PPE prote	probable PE protei	PPE	PPE	PPE	probable PPE prote		probable PPE prote
G70834	A70931	G70570	B70969	F70846	B70524	A70762	H70874	F70675	D70676	D70604	C70830	E70663	F70825	B70987	E70946
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12.8	12.6	12.5	12.4		12.2	12.2	12.2	12.1	12.0	12.0	12.0	11.9	11.7	11.6	r.

ALIGNMENTS

382 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQTAAQNGVRAMSSLGSSLGSSG	181	Qy 322 LLEGAAAVEEASDTAAANQLMNNVPQALQQPTQGTTPSSKLGGLWKTVSPHRSPISN 381	Db 121 LIAINLIGGNTPAIAVNEAEYGEMWAQDAAARGYAAATATATATLIFFEEAPEMTSAGG 180	Db 61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120	Qy 142 MVDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLIVGSWIG 201	Query Match Best Local Similarity 99.7%; Pred. No. 4e-92; Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	C;Ganetics: A;Gene: PPE	A;Residues: 1-391 <col/> A;Cross_references: GB:Z93777; GB:AL123456; NID:g3261726; PIDN:CAB07839.1; PID:e311073; i A;Experimental source: strain H37Rv	Astrucession: 57,0000 Astronus: preliminary; nucleic acid sequence not shown; translation not shown AsMolecule type: DNA	genome	Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
121 LIATNILIGGNIPALAVNEAENGEWAGDAAAMFGYAAATATATALLIFIFEEAPEMITSAGG 322 LLEQAAAVEEASDTAAANOLANNVPQALQQLAQPTQGTTPSSKLGGLWRTVSPHRSPISN [121 LIATNILGGNTPALAVNEAEYGEMWAQDAAAMFGYAATATATLLFFEEAPEMTSAGG 322 LLEQAAAVEEASDTAAANQLANNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN	121 LIATNILIGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLLFFEEAPEMTSAGG			1 MYDFGALPPEINSARMYARGFGSAGINUAAAQMWDSYASDIFSAASAFQSYYWGLTYGSWIG 202 SSAGLMYAAASPYYAMMSYTAGQAELTAAQYRYAAAAYETAYGLTYPPPYIAENRAELMI	142 MVDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFOSVVWGLTVGSWIG	Duery Match 52.7%; Score 1944; DB 2; Length 391; Best Local Similarity 99.7%; Pred. No. 46-92; 42 Mismatches 1; Indels 0; Gaps 142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVWGLTVGSWIG 20	Ch	293777; GB:AL123456; NID:G3261726; PIDN:CAB07839.1; PID:e311073; strain H37Rv 52.7%; Score 1944; DB 2; Length 391; 99.7%; Pred. No. 4e-22; 1; Indels 0; Gaps 0; vative 0; Mismatches 1; Indels 0; Gaps 0; H1	### ### ##############################	genome :
61 SSAGIMVAAASPYVAMMSVTAGQAELITAAQVRVAAAAYETAYGITVPPPVIABNRAELMI 262 LIATNLLGGVYPATAVNBAEYGEWWAQDAAAMFGYAAATATATLLPFEEAPENTSAGG [61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVYVAAAAYETAYGLTVPPVIJAENRELMI 262 LIATNLLGOATPAIAVNEAEYGEMWAQDAAAARSTATATATLLPPEEAPENRSAGG 121 LIATNLLGOATPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPPEEAPENRSAGG 121 LIATNLLGOATPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPPEEAPENTSAGG 322 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN	61 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPVIAENRELMI 262 LIATNLLGANTPAIAVNEEYGEMWAQDAAAMFGYAAATATATLLPPEEAPENRSAGG 	61 SSAGIMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGITVPPPVIAENRELMI 262 LIATNLLGQYNPAIAVNEAEYGEWWAQDAAMFGYAATATATATLLPFEEAPEMTSAGG		1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG	142 MVDFGALPPEINSARMYAQPGSASLVAAAQMWDSVASDLFSAASAFOSVVWGLTVGSWIG 	Duery Match 52.7%; Score 1944; DB 2; Length 391; Best Local Similarity 99.7%; Pred. No. 4e-92; Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 142 MVDFGALPPEINSARWYAGPGSASLVAAAQWMDSVASDLFSAASAFQSVVWGLTVGSWIG 20	ch 1 Similarity 99.7%; Score 1944; DB 2; Length 391; 1 Similarity 99.7%; Pred. No. 4e-92; 1390; Conservative 0; Mismatches 1; Indels 0; Gaps 42 MVDFGALPPEINSARWYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 20	293777; GB:AL123456; NID:G3261726; PIDN:CAB07839.1; PID:e311073; strain H37Rv 52.7%; Score 1944; DB 2; Length 391; 99.7%; Pred. No. 4e-92; vative 0; Mismatches 1; Indels 0; Gaps 0; vative 0; Mismatches 1; Indels 0; Gaps 0; EINSARMYAGPGSASLVAAAQWWDSVASDLFSAASAFQSVVWGLTVGSWIG 201	Ducleic acid sequence not shown; translation not shown 293777; GB:AL123456; NID:G3261726; PIDN:CAB07839.1; PID:e311073; 52.7%; Score 1944; DB 2; Length 391; 99.7%; Pred. No. 4e-92; vative 0; Mismatches 1; Indels 0; Gaps 0; VALIVE 0; Mismatches 1; Indels 0; Gaps 0; EINSARWYAGPGSASLVAAAQWWDSVASDLFSAASAFQSVVWGLTVGSWIG 201	genome ;11073;
202 SSAGLMVADASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	202 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI	202 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI	202 SSAGLMVADASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI	202 SSAGIMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENKAELMI		142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG	Duery Match 52.7%; Score 1944; DB 2; Length 391; Best Local Similarity 99.7%; Pred. No. 4e-92; Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 142 MVDFGALPPEINSARMYAGPGSASUVAAAQWMDSVASDLFSAASAFOSVWMGLTVGSWIG 20	ch 1 Similarity 99.7%; Score 1944; DB 2; Length 391; 390; Conservative 0; Mismatches 1; Indels 0; Gaps 42 MVDFGALPPEINSARWYAGPGSARVAAAQWMSVASDLFSAASAFQSVVWGLTVGSWIG 20	Strain H37Rv strain H37Rv strain H37Rv 52.7%; Score 1944; DB 2; Length 391; 99.7%; Pred. No. 4e-32; vative 0; Mismatches 1; Indels 0; Gaps 0;	nucleic acid sequence not shown; translation not shown 293777; GB:AL123456; NID:G3261726; FIDN:CAB07839.1; PID:e311073; 52.7%; Score 1944; DB 2; Length 391; 99.7%; Pred. No. 4e-92; vative 0; Mismatches 1; Indels 0; Gaps 0; vative 0; Mismatches 1; Indels 0; Gaps 0;	genome
Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Ebiology of Mycobacterium tuberculosis from the complete genome 500; MUID:98295987; PMID:9634230 mucleic acid sequence not shown; translation not shown mucleic acid sequence not shown; translation not shown 233777; GB:AL123456; NID:93261726; PIDN:CAB07839.1; PID:e311073; strain H37Rv 52.7%; Score 1944; DB 2; Length 391; 52.7%; Pred. No. 4e-92; EINSARWYAGPGSASLVAAAQWWDSVASDLFSAASAFGSVVWGLTVGSWIG 201 EINSARWYAGPGSASLVAAAQWWDSVASDLFSAASAFGSVVWGLTVGSWIG 60 ENSARWYAGPGSASLVAAAQWWDSVASDLFSAASAFGSVVWGLTVGSWIG 60 ENSPRYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261 ASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261 ASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120 NTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG 180 EASDTAAANOLANNVPQALQQLAQPTGGTTPSSKLGGLWKTVSPHRSPISN 381 ELILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	genome 11073;	genome 11073;	genome 11073;	genome ;11073;	genome	genome	genome	genome	genome		
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genome genome 11073;	rodon, 'Oyd,'	rodon, 'oyd,'	rrdon, royd, 111072	genom genom	oyd, oyd, genom	oyd,	oyd, oyd, genom	ordon, oyd, geno	ordon, toyd, genom	oyd,	<pre>D. ; Gordon, ; Holroyd, S.</pre>
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Gaps ., 9

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A;Gene: pepA
C;Superfamily: Bscherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps
                     A;Cross-references: GB:Z95390; GB:AL123456; NID:g3261766; PIDN:CAB08702.1; PID:e316074; A;Experimental source: strain H37Rv C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;
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A;Cross-references: GB:Z96071; GB:AL123456; NID:g3242254; PIDN:CAB09453.1; PID:g2181967 C;Genetics:
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable serine proteinase pepA - Mycobacterium tuberculosis (strain H37RV) C,Species: Mycobacterium tuberculosis C,Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision 17-Jul-1998 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SSAGLMADAAASPYVAWMSVTAGQAQLTAAQVRVAAAAXETAYRLTVPPPVIAENRTELMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MYDFGALPPEINSARMYAGPGSASLVAAAKMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTAAQNGVRAMSS----LGSSL
                                                                                                                                                                                                                                                                                                                            Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                 Query Match
42.9%; Score 1583; DB 2; 1
Best Local Similarity 81.5%; Pred. No. 9.7e-74;
Matches 322; Conservative 20; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532
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Best Local Similarity
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A; Recession: H70741
A; Residues: Preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-396 <COL>
A; Residues: 1-396 <COL>
A; Residues: 1-396 <COL>
A; Reperence GB:275555; GB:AL123456; NID:93261608; PIDN:CAA99966.1; PID:e250360; A; Genetics: PPE
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-011-1998 #sequence_revision 17-011-1998 #text_change 22-Oct-1999
C;Accession: C70568
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Natures 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Attiele: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: C70568
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                                                                                                                                                                                                                             probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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probable secreted serine proteinase [imported] - Mycobacterium leprae cispecies: Mycobacterium leprae cispecies: Mycobacterium leprae cispecies: Mycobacterium leprae cispecies: Mycobacterium leprae cispecies: Mycobacterium leprae cispecies: Mycobacterium leprae cispecies: Mycobacterium leprae cispecies: Mycole, S.T.; Elgimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1011, 2001
A,Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A,Attle: Massive gene decay in the leprosy bacillus.
A,Reference number: A66909; MUID:21128732; PMID:11234002
A,Reference number: A66909; MUID:2130332; PMID:11234002
A,Residue: 1-354 <STO>
A,Residues: 1-354 <STO>
A,Coss.references: GB:AL450380; NID:g13093863; PIDN:CAC32191.1; GSPDB:GN00147
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C;Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp¤
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Length 393;

Score 775.5; DB 2; Pred. No. 1.3e-32;

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Query Match Best Local Similarity

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A; Accession: B70931
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A;Residues: 1-409 <COL>
A;Cross-references: CB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17729.1; PID:e125461
A;Sxperimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Anture 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                            Cjacession: A70332
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Barish, M.S.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70932
A;Stelminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEQAAAVEEASDTAAA-----NQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 NGVR----AMSSL----GSSLGS-SGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARALPLTSLTSA-AERGPGOMLGGLPVGOMGARAGGGL----SGVLRVPPRPYVMPHSP 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ARQAVQTAAQ 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                        C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 409;
                                                          probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.4%; Score 753.5; DB 2;
larity 41.8%; Pred. No. 1.8e-31;
Conservative 52; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGSVTEDVASTTTIIVIPA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGDIAPPALSQDRFADFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184;
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Best Local 9
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PPE-damily protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001
C;Date: 20-Apr-2001
R;Cole, S.T.; Etglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R.; Davies, R.M.; Davlin, K.M.
Nature 409; 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq.
A;Reference number: As6909; MUID:21128732; PMID:11234002
A;Accession: H97056
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-423 «COL»
A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17722.1; PID:e1254612
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
                                                                                                                                                                                                                                                                                                                                          12;
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A;Residues: 1-421 <STO>
A;Residues: 1-421 <STO>
A;Croser-references: GB:AL450380; NID:g13093150; FIDN:CAC31563.1; GSPDB:GN00147
C;Genetics:
A;Gene: Mil182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 VPQAWAAANQAVTPAARALPLISLIS---AAERGPGQMLGGLPVGQMGARAGGGLSGVLR 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 201
                                                                                                                                                                                                                                                                                                                                                                                                        143 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 SSTSMASAAAPYVAWMSATAVHAELAGAQARLAIAAYEAAFAATVPPPVIAANRAQLMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 SKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQNGVRAMSSLGS------SLGSSGLGGG-VAANLGRAASVGSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 LEQAAAVEEASDTAAAN-----QLMNNVPQALQQLAQPT----QGTTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GVLPPSGVPYLLGIQSVL----
                                                                                                                                                                                                                                                                     20.0%; Score 737; DB 2; Length 423; 41.8%; Pred. No. 1.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 421,
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                                                                                                                                                                                                                                                                                                                                      Mismatches 125;
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qa	1 MFDFAALSPETNSTRWYLGPGSSPILTAAAAWVVLAKELTAAAQGLQSAVBAL-LTTFEG 59	RSPISNMVS
δ	202 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261	Db 244 WIDKLWALLDPNSNFWNTIASSGLFLPSNTIAPFLGLLGGVAAADAAGDV 293
Dβ	60 ESAAALAERVTPYEKWLTQNAASAELTATQLTVAANAYETAFTMTVPPLMVFVNRAQACL 119	419 VQTAAQNGVRAMSSLGSS-GLGGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAAR
<u>ک</u> و	262 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILPFEEAPEWTSAGG 321	DD 294 LGEATSGGLGGALVAPLGSAGGLGGTVAAGLGNAATVGTLSVPPSWTAAAPLASFLGS 351 QY 478 ALPLTSLTSAAERGPGQMLGGLPVQQMGARAGGGLSGVLRVPPRPYVMPHSPA 530
λ O Q	322 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQP 355	Db 352 ALGGTPMVAPPPAVAAGMPGMPFGTMGGQGFGRAVPQYGFRPNFVARPPA 401 Oy 531 AG 532
% व	413	Db 402 AG 403
\ \delta = \frac{1}{2}	AARQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAAN 469 THE	RESULT 12 G70925 probable PPE protein - Mycobacterium tuberculosis (strain H37RV) C.Species: Mycobacterium tuberculosis
o d	OAVTPAARALPLISLISAAERGPGQML-GGLPVGQMGARAGGGLSGVLRVPRRYVM 525	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: G70925. R;Cole, S.T; Brosch, R; Parkhill, J; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;Cole, S.T; Brosch, R.; Devlin, K.; Feltwell, T.; Genles, S.; Hamlin, N.; Holroyd, S.;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Genles, S.; Hamlin, N.; Holroyd, S.
S d	526 PHSPAAG 532 : 415 PRNPAAG 421	Rajdiarem, A.M.; A.M.; A.M. A.M. A.M. A.M. A.M. A.
RESULT		A; Relection = number: A/0500; NOID: 3525350; Final States = A; Accession: G70525; Nucleic acid sequence not shown; translation not shown A; Status: preliminary; nucleic acid sequence not shown; translation not shown a solution into
probabl C;Speci C;Date: C;Acces		A; Construction of the Con
R;Cole, ; Conno Rajandra Nature : A:Autho	Gordon, olroyd, S	Ajvene: FFE Query Match 19.0%; Score 702; DB 2; Length 408; Best Local Similarity 42.3%; Pred. No. 7.4e-29. Matches 180; Conservative 48; Mismatches 144; Indels 54; Gaps 13;
A;Title A;Refer A;Acces: A;Status	. Deciphering the biology of Mycobacterium tuberculosis from the complete genome ence number: A70500; MUID:98295987; PMID:9634230 sion: H70931 sion profilminary, nucleic acid sequence not shown; translation not shown	INSARMYAC INSGRMYAC
A, Molec A, Resid A, Cross A, Exper	olecule type: DNA esidues: 1-403 <col/> ross-references: GB:AL022021; GB:AL123456; NID:G3250699; PIDN:CAA17728.1; PID:e125461 xperimental source: strain H37Rv	CY 203 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPFPVIAENRAELMIL 262
C;Genet A;Gene:	C;Genetics: A;Gene: PPE A;Gene	QY 263 IATNILGONTPALAVNEAEYGEMWAQDAAMFGYAAATATATALLPFEEAPEMTSAGGL 322
Best	Indels	323 LEQARAVEBASDTARANQLMINVPQALQQ-LAQPTQGTTPSSKL
λ O O	143 VDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFOSVVWGLIVGSWIGS 202	STSLIPWYSALQOWLAENLI ANNHMSMINSGVSMINTLSS
δ d	203 SAGIMVAAASPYVAWMSVTAGGAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 262 ::	DD 240 RLIGISYFDEGLLQFEASLAQQAIPGTPGGAGDSGSSVLDSWGPTIFA 287 Qy 414 AARQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAAN 469
8 8		Db 288 GPRASPSVAGGGAVGGVQTPQPYWYWALDRESIGGSVSAALGKGSSAGSLSVPPDWAARA 347
} & :	LEQARAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSS	348
අ <u>ග</u>	184 AAQSAAIAHATGASAGAQQTTLSQLIAAIP8VLQGLSSSTAATFASGPSGLLGIVGSGSS 243	Oy 527 HSPARG 532

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Gordon, S.
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A;Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17730.1; PID:e125462(
A;Experimental source: strain H37Rv
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Accession: B70625
A; Accession: B70625
A; Molecule type: DNA
A; Residues: 1-391 < COL>
                                                                       A, kesiques: 1-391 <COL>
A, by cross-references: GB: 292539, GB: All 23456; NID: G3261714; PIDN: CAB06873.1; PID: e304546; C, Genetics: A cource: strain H37Rv C, Genetics: A, Genetics: A, Genetics: A, Genetics: A
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C;Species: Mycobacterium tuberculosis

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: B70932

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Peltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Equares, S.

Nature 393, 537-544, 1998

A;Atther: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MuID:98295987; PMID:9634230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P--ISNMVSMANNHMS-MINSGVSMINTLSSMLKGFAPAAARQAVQTAAQNGVRAMSSLG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQ 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary, nucleic acid sequence not shown, translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ASMANVADAQPYLAWLTYTAEAAHAGSQAMASAAAYEAAYAMTVPPEVVAANRALLAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IATNILIGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGL
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                                                                                                                                                                                                                                                                                                                                                                                           14; Gaps
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                                                                                                                                                                                                                                                                                                                            Query Match
18.9%; Score 697; DB 2; Length 391;
Best Local Similarity 42.1%; Pred. No. 1.3e-28;
Matches 165; Conservative 62; Mismatches 151; Indels
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18.7%; Score 689; DB 2; Length 46:
Best Local Similarity 38.4%; Pred. No. 4e-28;
Matches 174; Conservative 66; Mismatches 147; Indels
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                                                                                                                                              probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 1.-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70660
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MulD:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:295436; GB:AL123456; NID:g3261770; PIDN:CAB08826.1; PID:e316565; A;Experimental source: strain H37Rv C;Genetics: A;Gene: PPE
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C;Species: Mycobacterium tuberculosis
C;Decies: Mycobacterium tuberculosis
C;Dacession: B70622
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Perkhill, M.; Felewell, T.; Gentles, S.; Hanlin, N.; Holroyd, S; Calandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIATNILIGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATTLIPFEEAPEMTSAGG 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-413 <COL>
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Best Local Similarity 39.1%
Matches 168; Conservative
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203 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 262 	263 IATNILGONTPAIAVNEAEYGEMMAQDAAMFGYAAATATATTLPFEEAPEMTSAGGL 322 	323 LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGL- 368	369WKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAÞAARQ 417 238 NAIFGPTGATTYQNVFVTAANVTKFSTWANDAMSABNLGMTEFKVFWQPPPAPE 291	418 AVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAV 472	473 TPAARALPLISLISA-ABRGFGQMLGGLPVGQMGARAGGGLSGVLRVPPRFYVWPHSPAA 531 	532 GDIAPPALSQDRFADFPALPLDPSAMVAQVGPQ 564 :
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Search completed: June 30, 2004, 16:54:00 Job time: 20.0527 secs

Wed Jul

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 30, 2004, 16:42:21; Search time 11.8689 Seconds (without alignments) 3198.204 Million cell updates/sec

US-09-597-796C-12 3686 1 MHHHHHHTAASDNFQLSQGG.....SGGPVVNGLGQVVGMNTAAS 729 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description						Q10540 mycobacteri						O06246 mycobacteri		arabi		P31137 escherichia	Q9z6t0 chlamydia p		P39099 escherichia		bacillu			Q44597 brucella su		mycobact	haemo		lactob	Q92jal rickettsia	P15502 homo sapien	Q8yg32 brucella me	P26982 salmonella
	EI.	61 M	YS92_MYCTU	Y102_MYCTU	YF48 MYCTU	Y442 MYCTU	Y878 MYCTU	SRA MYCLE			Y096_MYCTU		YY29 MYCTU	HRA2 HUMAN						DEGO_ECOTI	HRA2 MOUSE	HTRA_BACSU				DEGP_BUCAI		HTOA HAEIN			DEGP_RICCN	1	ומו ומו	DEGP_SALTY
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Q9fec4 chlamydomon P04985 bos taurus P09376 escherichia P18584 chlamydia t P35828 caulobacter O85291 buchnera ap Q9p197 chlamydia m Q55894 rhizobium m O55942 rickettsia P15921 rickettsia P54925 bartonella P12021 sus scrofa
RAA3 CHLRE ELS BOVIN DEGE ECOLI DEGP CHLTR DEGE CHLTR DEGE CHLTR DEGE CHLMU DEGE CHLMU DEGE RICER OMPA_RICRI DEGE BARHE APMU_PIG
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MEDINE=98295987; Pubmed=9654230;
MEDINE=98295987; Pubmed=9654230;
Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1999).
                                                                                                                                              1 MYDFGALPPEINSARMYAGPGSASLVAAAKMWDSVASDLFSAASARQSVVWGLTTGSWIG
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                                                                                               Gaps
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                                                                                             7;
                                                                    DB 1; Length 396;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                             34; Indels
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15-DEC-1998 (Rel. 37, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv2892c/MT2959/Mb2916c.
Rv2892C OR MT2259 OR MTCY274.23C OR MB2916C.
Mycobacterium tuberculosis, and
                          A -> AT (IN REF. 2).
6AFAE0D7B5F668D0 CRC64;
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                                                                 44.9%; Score 1656.5; DB larity 85.1%; Pred. No. 2.4e-74; Conservative 18; Mismatches 34
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Pfam; PF00823; PPE; 1.
Hypothetical protein; C
CONFLICT 158 159
                                                                   Query Match
Best Local Similarity
Matches 338; Conserv
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Q10813;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EVRL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPECIES=M.Dovis; STRAIN=AF2122/97;
SPECIES=M.Dovis; STRAIN=AF2122/97;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
"The Complete genome sequence of Mycobacterium bovis.";
"The SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity. 42.3%; Pred. No. 9.7e-28;
Matches 180; Conservative 48; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculist; Rv2892c; -.
InterPro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 56 76
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3E3D1F20D7827199 CRC64;
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or send an email to license@isb-sib.ch).
                                                                                                                                                                             Bacteriol. 184:5479-5490(2002)
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EMBL; AE007119; AAK47285.1; -.
EMBL; BX248344; CAD96603.1; -.
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Gaps

49;

DB 1; Length 463;

Score 687.5; DB Pred. No. 5.7e-27

18.7%; 42.8%;

46021 MW; EE64828BF09FA551 CRC64;

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Matches 174; Conservative
463 AA;
                                       Local Similarity
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01-0CT-1996 (
15-JUL-1999 (
10-0CT-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22506494; PubMed=122180365,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman U.A., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                             SPECIES=M.tuberculosis, STRAIN=H37Rv,
MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=98282; Barris C., Harris Gordon S.V., Biglmeier K., Garris S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Khillingworth T., Connor R.,
Badcock K., Berlwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., MoLean J., Moule S., Murphy L.,
Oliver S., Oseger K., Skelton S., Squares S., Squares R.,
Bulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                    Harris
                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                   30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1802/MT1851/Mb1830.
RV1802 OR MT1851 OR MTV049.24 OR MB1830.
Mycobacterium tuberculosis, and
Mycobacterium bovis.
                                                                                                                                                                                                      Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                         463 AA
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InterPro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Complete proteome.
CONFLICT 401 401 S -> L (IN
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                                                                                       30-MAY-2000 (Rel. 39, Created)
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                                                         STANDARD;
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                                                         MYCTU
                                         YIO2_MYCTU
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322
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                                                                                                                                                                                                                                                                                                      60 SSGTMAAAAAPYVAWMSATAALAREAAAQASAAAAAYEAAFAATVPPPVVAANRAELAVL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 NSMLGLGFAESKAVLPANDTVISTIFGWVQFQKFFNPVTPFNP------DLIP
                                                                                                                      143 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                             203 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Sten J.A., Carpenter L., White O.,
Feterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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48; Mismatches 136;
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15-UUL-1999 (Rel. 38, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1548c/MT1599.
RV1548C OR MT1599 OR MTCY48.17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 12.2%; Score 450; DB 1; Length 678; al Similarity 26.5%; Pred. No. 3.4e-15; 155; Conservative 70; Mismatches 209; Indels 150; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 VDFGALPPEINSARMYAGPGSASIVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASAAMTGVAASYARWLTTAAAQAEQAAGQAQAAVSAFEAALAATVHPGAVSANRGRLRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 NAVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTAAQNGVRAMSSLGSSLGSS
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laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete protecme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 D -> G (IN REF, 2).
66736 MW; 209F1593D52533A2 CRC64;
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Interpro; IPR002899; Myccobac pentapep.
Pfam; PF01469; Pentapeptide_2; 11.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE007026; AAK45866.1; ALT_INIT.
PIR; A70762; A70762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein;
TRANSMEM 14 34
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678 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                        Harris D.
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MEDLINE-22266494; PubMed=12218036;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Hokey E.,

Rolonay J.F., Nelson W.C., Umayam L.A., Ermclaeva M., Salzberg S.L.,

Bishai W., Jacobs W.R. Jr., Weidman J., Khouri H., Gill J., Mikula A.,

Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;

"Whole-genome comparison of Mycobacterium tuberculosis clinical and

laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Bashama D., Brown D., Chillingworth T., Connor R., Horneby T., Jagels K., Kregh A., McLean J., Moule S., Hamlin N., Horreyd Horneby T., Jagels K., Kregh A., McLean J., Moule S., Murphy L., Chilter S., Seeger K., Skelten S., Rajandram M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Shelten S., Barrell B.G.; Complete genome sequence: "Mycobacterium tuberculosis from the Nature 193:537-544 (1999).
                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                        10 65-kilodalton antigen of Mycobacterium tuberculosis.";
10 88cteriol. 169:1080-1088 (1987).
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I -> T (IN REF. 1).
G -> GNNNIG (IN REF. 1).
; 97234D5B316C8C7F CRC64;
                                                  16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv0442c/MT0458
MY0442C OR MT0458 OR MTV037.06C.
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InterPro; IPR002989; Mycobac_Dentapep.
Pfam; PF01469; Pentapeptide_2; 5.
Pfam; PF00823; PPE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                       STRAIN=Erdmann;
MEDLINE=87137260; PubMed=3029018;
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             P42611; 053727;
01-NOV-1995 (Rel. 32, Created)
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EMBL; AE006948; AAK44681.1; -...
PIR; C70830; C70830.
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                                                                                                                             Mycobacterium tuberculosis.
STANDARD;
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MYCTU
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                                                                                                                                                                                                                                                                 TNLLGGNTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAG---- 320
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                                                                                                                                                                                                                                                                                                                                                          321 --GLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLG------GLW
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                                                                                                6 FAWLPPEINSALMFAGPGSGPLIAAATAWGELAEELLASIASLGSVTSELTSGAWLGPSA
                                                                                                                                                                     205 GLWVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 LTSLTSAAERGPGQM-----LGGLPVGQMGARAG--GGLSGVLR--VPPRPYVMPHSPAA
                                                                       145 FGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSA
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MEDINE=22206494; White O.,
REDINE=22206494; PubMed=12218036;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umwayam L.A., Ermouri H., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Lr., Venter J.C., Fraser C.M.;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Bardon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Dadcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentless S., Haminn N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Allorer S., Seeger K., Skelton S., Squares R., Squares R., Squares R., Squares R., Shelton S., Squares S., Squares R., Sulter S., Betology of Mycobacterium tuberculosis from the complete genome sequence.";
                            58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 NTGSGNIGFGITGDHQMGFGGFNSGSGN-IGFGNSGTGNVGLFNS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteriaes, Actinomycetales, Corynebacterinese, Mycobacteriaceae, Mycobacterium.
  ; Pred. No. 4.1e-15;
49; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0cT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv0878c/MT0901.
RV0878C OR MT0901 OR MTCY31.06C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443 AA
  31.9%;
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                              Matches 135; Conservative
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       Best Local Similarity
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Y878 MYCTU
AC Q10540,
DT Q10-CT-1996
DT 10-CCT-1996
DT 10-CCT-2003
DE HYPOCHETICAL
GN KV0878C OR M
OS MYCODACTERIOR
OC COCYNEDACTERIOR
OC NCBI TAXID=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVG---SW
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Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                  Transmembrane; Repeat; Complete proteome.
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C58BEC607F0675E2 CRC64;
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
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ALA-RICH.
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InterPro; IPR002989; Mycobac Pentapep.
Pfam; PF01469; Pentapeptide_2; 4.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z73101, CAA97385.1; -.
EMBL, AE006977; AAK45143.1; ALT_INIT.
PIR, C70780; C70780.
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181
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443 AA;
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16-OCT-2001 (
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SRA_MYCLE
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=9323928; Pubmed=8478104;
Wega-Lopez F., Brooks L.A., Dockrell H.M., de Smet K.A.L.,
Thompson J.K., Hussain R., Stoker N.G.;
"Sequence and immunological characterization of a serine-rich antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruthers S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A Mycobacterium leprae-specific gene encoding an immunologically recognized 45 kDa protein.";
Mol. Microbiol, 10:829-838(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95020554; PubMed=7934845;
Rinke de Wit T.F., Clark-Curtiss J.E., Abebe F., Kolkon A.H.J.,
Jonson A.A.M., Thole J.E.R.;
                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00823; PFE; 1.
Antigen; Repeat; Complete proteome.
DOMAIN 192 196 POLY-SER.
192 255 2 X 6 AA REPEATS OF S-V-A-Q-S-E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n 9.8%; Score 363; DB 1; Length 408; Similarity 26.2%; Pred. No. 3.4e-11; Conservative 73; Mismatches 169; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wature 409:1007-1011(2001).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T -> S (IN REF. 2).
S -> L (IN REF. 2).
H -> D (IN REF. 2).
P -> L (IN REF. 2).
F -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
      (45 kDa protein)
                                                                                                                                                                                                                                                                                                                                                                                                                     Infect. Immun. 61:2145-2153(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leproma; ML0411; -.
InterPro; IPR000030; Microbac_PPE
Pfam; PF00823; PPE; 1.
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EMBL; X66431; CAA48480.1; -.
EMBL; Z21952; CAA79950.1; -.
EMBL; Z97179; CAB09338.1; -.
EMBL; ALS83918; CAC29919.1; -
   Serine-rich antigen (25L) (4)
SRA OR ML0411 OR MLCL383.14.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                             from Mycobacterium leprae.
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EMBL; AL583318; CAC299
PIR, CA6960; C86960.
PIR; S33522; S33522.
PIR; S39872; S39872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Best Local Simi
Matches 117;
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                                                                                                                                                                                                                                                                                      262 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLIPFEEAPEMTSAGG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 CMDRRDSVNSFHSSSSSDSLYESIDNLYDSVAQSEBHGSDSMSQSYNTCGSVAQSELCDS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 ASSIM----PIVASQVTETLGRSQV-AVEKMIQSISSTAVSVDVAASKVVAGGAVSQAVSVG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381
142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 201
                                                                         9
                                                                 1 MFDFMVYSPEVNAFLMSRGPGSTPLWGAAEAWISLAEQLMEAAQEVSDTIVVAVPASFAG
                                                                                                                                                                                         61 ETSDMLASRVSTFVAWLDGNAENAGLIARVLHAVAYAFEBARAGMVPLLTVLGNIIHTWA
                                                                                                                                           202 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 PFGTPSQSSQSNDLSATSLTQQLGGL-----DSIISSASASLLTTNS--ISSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PTQ-----GTTPSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 ISSMLKGFAPAARQAVQTAAQNGVRAMSSLGSSLGSSGLGGGGVAAN----LGRAASVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458 SLSVPQAWAAANQAVTPAARALP--LTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGV
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MEDLINE-22206494; PubMed=12218036;
MEDLINE-22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nalson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher J. V. Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Lr., Venter J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; Parkhill U., Garnier T., Churcher C., Harris I Gordon S. V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S Hornsby T., Jagels K., Krodh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton A., Rajandream M.A., Rogers J., Stutter S., Seeger K., Skelton S., Squares R., Stutter S., Sularres R., Stutter S., Sularres R., Mitchend S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                         322 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQ-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             516 LRVPPRPYVMPHSPAAGD-IAPPALSQ 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 TQ--PAREVLTASVAGGSGTGGPAFNE 406
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12;

Gaps

88;

169; Indels

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435

PRT;

STANDARD;

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053268; 053269;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SAMSS Institute of Bioinformatics and the EMBL outstands. The the EUROpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGSSL------GSSGLGG--GVAA--NLGRAASVGSLSVPQAWAAANQAVTPAARA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 LGGPLLGALAAAVVPGVAGLAGVAGLAALPAVGAAAGAPAALVGSVAPVSGGVVSPQAR- 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAVEEASDTAAAN------QLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ANEASNAVAAATITPFPWHEIVQFLEETFAAYDQYLSALLSELPA--VAWVWFQLFVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 ILGFNIIGFIITLASNAQLLTEFAINASYVAVGLLYAIA-GVIDIVVEWVIGNLFGVVPL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KESVGOPAG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVAAYVPYVAWLVQASADSAAAAGEHEAAAAGYVCALAEMPTLPELAANHLTHAVLVATN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                  reductase.
CAUTION: Ref.3 sequence differs from that shown due to frameshifts
in positions 294; 337 and 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 LPLTSLTSAAERGPGOMLGGLPVGOMGARAGG--GLSGVLRVPPRPYVMPHSPAAGDIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASPPEVHSALLSAGPGPGSLQAAAAGWSALSAEYAAVAQELSVVVAAVGAGVWQGPSAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQTAAQNGVRAMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 ALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                        STRAIN=Isolate 50410,

Backi A.H., Dale J.W.;

Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to the mycobacterial PPE family.

-!- CAUTION: In strain Oshkosh the gene for this protein is interrupted in position 307 by an ISG110 element.

-!- CAUTION: Was originally (Ref.3) thought to be a dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                           9.2%; Score 338; DB 1; Length 43 27.2%; Pred. No. 6.1e-10; Live 54; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    al protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LVSAVEPAPASTSVSVLASDRGAGALGFVGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             537 PALSQDRFADFPALPLDPSAMVAQVGPQVVNI 568
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                                                                                                                                                                                                                                                                                EMBL, AE007129; AAK47427.1; ALT SEG.
EMBL, AE007129; AAK47430.1; ALT SEG.
EMBL, X59271; CAA41961.1; ALT FRAME.
PIR, E70857; E70857.
                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR000030; Microbac_PPB.
Pfam; PF00823; PPB; 1
Hypothetical protein; Complete pro
SEQUENCE 434 AA; 43029 MN; 411
                                                                                                                                                                                                                                                                         EMBL; AL021287; CAA16103.1; -.
 [3]
SEQUENCE OF 160-374 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Tuberculist; Rv3018c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                       TIGR; MT3098;
TIGR; MT3101;
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tive 59; Mismatches 172; Indels 133; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22206494; PubMed=12218036; Risen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Eath D., Hackey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J.A., Khouri H., Gill J., Mikula A., Blishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M., "Whole-genome comparison of Mycobacterium tuberculosis clinical and
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MEDLINE 98295987; PubMed=9634230;

Cole ST., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Devlin K., Feltwell T., Gentles S., Hamiin N., Holroyd Hornsby T., Jaqels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Seeger K., Skelton S., Squares S., Squares R., Stalton J.E., Taylor K., Whitchead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
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                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-i- SIMILARITY: Bactongs to the mycobacterial PPE family.
-i- CAUTION: Ref.1 sequence differs from that shown due to
                                16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein RV3021c/RV3022c/MT3106.
RV33021C/RV3022C OR MT3106 OR MTV012.35C/MTV012.36C.
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LAGV -> VTGL (IN REF. 2).
L -> V (IN REF. 2).
                             update)
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EMBL; AL001287; CAA16107.1; ALT_FRAME.
EMBL; ABCO07129; AAK47435.1;
TIOR: MT3106;
Tuberculist; Rv3021c;
Tuberculist; Rv3021c;
Tuberculist; Rv3022c;
Tuberculist; Rv3023c;
Fr06823; PPE;
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16_OCT-2001 (Rel. 40, Created)
16_OCT-2001 (Rel. 40, Last seg
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                                                                                                                                                                          Mycobacterium tuberculosis.
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CONFLICT 317 320
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RESULT 9 YU21_MYCTU

CC This SWILARITY: Belongs to the mycobacterial PPE family. CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- CC the European Bioinformatics Institutions as long as its content is in no way complified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ CC modified and mail to license@isb-sib.ch). EMBL; Z74410; CAA98932.; CR EMBL; Z74411; CAA98932.; CR EMBL; Z74410; CAA98932.; CR EMBL; Z74410; CAA98932.; CR EMBL; Z74410; CAA98932.; CR EMBL; Z74410; CAA98932.; CR EMBL; Z74410; CAA98932.; CR EMBL; Z74410; CAA98932.; CR EMBL; Z7410; C	Query Match 9.0%; Score 331; DB 1; Length 463; Best Local Similarity 25.2%; Pred. No. 1.4e-09; Matches 137; Conservative 64; Mismatches 197; Indels 146; Gaps 17;	ALPPEINGARMYAGPGSASIVAAAQWMDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGL 206 ALPPEINGARMYAGPGSASIVAAAQWMDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGL 206 ALPPEVHSGLLSAGCGFGLLLVAAQQWQELSDQYALACAELGQLGEVQASSWQCTAATQ 61 WAAAASPYVAWMSVTAGQAELTAAQVRVAAAATETAYGLTVPPPVIAENRAELMILLATN 266	
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Wed Jul

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RRAINLES BO044033; PubMed=9384377;

RA MEDLINE=98044033; PubMed=9384377;

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MOONE D., Howell A., Collery R., Devine K.M.;
"YkdA and YvtA, HtrA-like serine proteases in Bacillus subtilis,
"YkdA and YvtA, Guto-e autorisegulation and reciprocal cross-regulation of
ykdA and yvtA gene expression.";
J. Bacteriol. 183:654-663(2001).
-!- FUNCTION: May be involved in processing, maturation, or secretion
of extracellular enzymes.
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                       YYTA BACSU STANDARD; PRT; 458 AA. Q9R9II; 035039; 28-FBB-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Probable serine protease YVLA CR YYBE OR SSU33000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20158875; PubMed=10692364;
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-!- SUBCELLULAR LOCATION: Membrane-bound (Potential):
-!- INDUCTION: Induced by heat shock during exponential growth and by heterologous amylases at the transition phase of the growth cycle. Negatively regulates its own expression.
-!- MSCELLAMSOUS: Inactivation results in compensating overexpression of htth, especially during stress conditions.
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains I PDZ/DIR domain.
-!- GAUTION: Ref. 2 and Ref. 3 sequences differ from that shown due to frameshifts in positions 87 and 246 that produce two separate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|| | :|| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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PROSITE; PS50106; PDZ; 1.
Hydrolase; Protease; Serine protease; Heat shock; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
77551045546545CD CRC64;
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 CY
92 PC
458 EX
440 PD
187 CH
217 CH
298 CH
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DOMAIN 12
TRANSMEM 72
DOMAIN 93 4
DOMAIN 356 4
ACT SITE 187 1
ACT SITE 298
SEQUENCE 458 AA;
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93
356
187
217
298
458 AA;
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YY29 MYCTU
ID YY29 MYCTU
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STANDARD;

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321 G 321
                                      177 G 177
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Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
Nature 393:537-544(1998).
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                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BBE1FC025ABFBEA6 CRC64;
                                                                                                                                                                      Corynebacterineae; Mycobacteriaceae; Mycobacterium
NCBI_TaxID=1773;
               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypochetical PPE-family protein RV3429/MT3533
RV3429 OR MT3533 OR MTCY77.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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SEQUENCE 178 AA; 19811 MW; 8BE1FC025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000030; Microbac_PPE
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE007158; AAK47873.1;
PIR; C70975; C70975.
                                                                                                                           Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

Maraberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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MEDLINE=20453195; PubMed=10995577;
Raccio L., Fusco C., Viel A., Zervos A.S.;
Tissue-specific splicing of Omi stress-regulated endoprotease leads to an inactive procease with a modified PDZ motif.";
Genomics 68:343-347(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20428457; PubMed=10971580;

MEDLINE=20428457; PubMed=10971580;

Gray C.W., Ward R.V., Karran E.H., Turconi S., Rowles A.,

Viglienghi D., Southan C., Barton A., Fanton K.G., West A.,

Savopoulos J.W., Hassan N.J., Clinkenbeard H., Hanning C.,

Amegadzie B., Davis J.B., Dingwall C., Livi G.P., Creasy C.L.;

Characterization of human HrrA2, a novel serine protease involved in mammalian cellular stress response.";

Eur. J. Biochem. 267:5699-5710(2000).
                                                                                                                                                                                                                  (EC 3.4.21.-) (High
HRA2 HUMAN STANDARD; PRT; 458 AA.
043464; Q9HBZ4; Q9POY3; Q9POY4;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 40, Last annotation update)
Scrinc protease HTRA2, mitochondrial precursor (BC 3.4.21.-) (High emperature requirement protein A2) (HtrA2) (Omi stress-regulated endoprotease) (Serine proteinase OMI).
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Faccio L., Fusco C., Chen A., Martinotti S., Bonventre J.V., Zervos A.S.,
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MEDLINE=20112822; PubMed=10644717;
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A. (ISOFORM 2).
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48840 MW;
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Almeri E.S., Shi Y.;

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Almeri E.S., Shi Y.;

Almeri E.S., Shi Y.;

Almeri E.S., Shi Y.;

Almeri E.S., Shi Y.;

Almeri E.S., Shi Y.;

Bructural insights into the pro-apoptotic function of mitochondrial serine protease HrAJ/Omi ";

Bructural insights into the pro-apoptotic function of mitochondrial serine protease HrAJ/Omi ";

Bructural insights into the pro-apoptotic function of mitochondrial serine protease HrAJ/Omi ";

Bructural insights into the pro-apoptotic activity against a nonspecific substrate beta-casein. Promotes or induces cell activity adainst a nonspecific substrate beta-casein. Promotes or induces cell an object individual protease or induces cell increase in caspase activity, or by a BIRC inhibition-independent mechanism. Isoform 2 seems to be proteolytically inactive.

C. SUBUNIT: Interacts with Mxi2. The mature protein, but not the precursor, binds to BIRC2, arRC3 and BIRC4/MIAP.

C. SUBUNIT: Interacts with Mxi2. The mature protein, but not the intermembrane space. Released into the cytosol following apoptotic stimuli, such as UV treatment, and stimulation of mitochondrial with Mitochondrial precommants aspase-8 truncated BID/tBID.

C. HATERNATIVE PRODUCTS:

Brant_Alternative splicing, Named isoforms-4;
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                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE=20334437; PubMed=10873535;
Savopoulos J.W., Carrer P.S., Turconi S., Pettman G.R., Karran E.H.,
Gray C.W., Ward R.V., Jenkins O., Creasy C.L.;
"Expression, purification, and functional analysis of the human serine procease HtrA2.";
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ALA-134.

BEDLINE-1468395; PubMed-11583623;

Suzuki Y., Imal Y., Nakayama H., Takahashi K., Takio K., Takahashi Suzuki Y., Imal Y., Imakayama H., Takahashi Maraki Y., Imal Y., Imal Y., Imal Y., Isleased from the mitochondria and interacts with XIAP, inducing cell death.";

Mol. Cell 8:613-621(2001).
 Generation and initial analysis of more than 15,000 full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=2; Synonyms=D-Omi;
IsoId=043464-2; Sequence=VSP_005359, VSP_005361;
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IsoId=043464-3; Sequence=VSP_005360, VSP_005361;
                   human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 134-458
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IsoId=043464-1; Sequence=Displayed;
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EMBL, AF141305, AAF66596.1; -.
EMBL, AF141306, AAF66597.1; -.
EMBL, AF141307, AAF66591.1; -.
EMBL, AF184911; AAG13126.1; -.
EMBL, AF184911; AAG13126.1; -.
EMBL, BC000066; ANOTANOTATED_CDS.
EMBL, BC000066; ANOTANOTATED_CDS.
PDB, 1LCY; 29-MAY-02.
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411 APAAARQAVQTAAQNGVRAMSSLGSSGLGGGGVAANLG---RAASVGSLSVPQA--- 464 465 -----WAAANQAV-----TPAARA----LPLTSLTSAAERGPGQMLGGLPVGQ 503 52 YGTPSLWARLSVGVTEPRACLTSGTPGPRAQLTAVTPDTRTREASENSGTRSRAWLAVA- 110 504 MGARA-----GGGLSGVLRVPPRPYVWPHSPAAGDIAPPALSQDRF---ADFPALPLD 553 SVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIG--GGVAVGEPVVAMGNSGGQGG 666 / FILEWAYE.
DGEVIGWAYER/TAGISFAIPEDBRIREFIHRGEKKNSSGI
SGSORRYIGWMLTLSPSILAELQLREPSFPDVQHGYLIHK
VILGBSPHRAGLERGDVILAGTGEWGWOALBDVFARTRINGSQ
LAVQIRRGRETLILLVYPEFUTE -> VSETGFLPRIPAGG
CGKGRPPLIGGCLWKPLSSSILAISQYPTRSPQHLLVLFG
CPHPLLFV (in isoform 4)..
/ FILEWS 005362.
A -> M: LOSS OF INTERACTION WITH BIRC4;
LOSS OF INHIBITION OF BIRC4 ACTIVITY.
A -> M: LOSS OF INTERACTION WITH BIRC4 AND
OF INHIBITION OF BIRC4 ACTIVITY.
S -> A: LOSS OF PROTEASE ACTIVITY.
S -> A: LOSS OF PROTEASE ACTIVITY.
NW; CEA955ATDODDBCOD CRC64; 3 APRAGR-----GIRWGRRPRLTPDLRALLTSGTSDPRARVT 111 IGAGGAVILILMGGG-----RGPPAVLAAVPSP-----PPASPRSQYNFIAD-----554 PSAMVAQVGPOVVNI----NTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAF 86; Gaps with bursts bursts and the control of the control o (in isoform 2 and isoform 3) L -> LARELGAVSLQ (in isoform 3). /FTId=VSP 005360. 6.2%; Score 228; DB 1; Length 458; 28.8%; Pred. No. 0.00015; tive 42; Mismatches 129; Indels 8 (in isoform 2). SERINE PROTEASE HTRA2 SYSTEM. CHARGE RELAY SYSTEM. CHARGE RELAY SYSTEM. CHARGE RELAY SYSTEM. IAP-BINDING MOTIF. POTENTIAL. SERINE PROTEASE. MITOCHONDRION.

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IsoId=Q99372-1; Sequence=Displayed;
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667 TPRAVPGRVVA-LGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGNN 725
                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Protease Do-like 8, chloroplast precursor (EC 3.4.21.-).
DEGPB OR ATGG19830 OR K13H13.1.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II, Brassicales; Brassicaceae, Arabidopsis.
NIBI_TAXID=3702;
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InterPro; 1PR001478; PDZ.
InterPro; 1PR001478; PDZ.
InterPro; 1PR001478; PDZ.
InterPro; 1PR001478; PDZ.
Pfam; PP00595; PDZ; 1.
Pfam; PF00895; PDZ; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; TALSE NEG.
Hydiciase; Serine procease; Transit peptide; Chloroplast; Thylakoid.
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-cv. Columbia; Kissalbach T., Systedt M., Schroeder W.P.; Submitted (OCT-2000) to Swiss-Prot. -!- FUNCTION: Probable serine protease. -!- SUBCELLUIAR LOCATION: Chloroplast; within the thylakoid lumen
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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CHARGE RELAY SYSTEM (POTENTIAL).
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CHARGE RELAY SYSTEM (POTENTIAL).
A986FC1387670AFF CRC64;
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PROTEASE DO-LIKE 8.
SERINE PROTEASE.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91104868; PubMed=1702999;
Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
Biochemistry 29:677-983(1990):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3] SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                   79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing, Named isoforms=8, Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                     566 VNI----NTKLGYNNAV----GAGTGIVIDPNGVVLTNNHVIAGATDIN----
6.1%; Score 225.5; DB 1; Length 448; 28.1%; Pred. No. 0.0002; tive 41; Mismatches 103; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 781-864 FROM N.A.
MEDIINE=88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
"Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.";
J. Biol. Chem. 263:13504-13507(1988).
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01-0cT-1996 (Rel: 34, Last sequence update)
10-0cT-2003 (Rel: 42, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
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                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 AKAAKYAGAGGGGVLPGVGGGGIPGGAGAIPGIGGITGAGTPAAAAAAAAAAAAAKAAKYGAA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIVAAAQMWDSVASDIFSAASAFQSVVWGLTVGSW----IGSSAGLMVAAASPYVAWMSV 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 and isoform 8).
/FTId=VSP 004244.
Missing (In isoform 3, isoform 5, isoform 6 and isoform 8).
/FTId=VSP 004245.
Missing (In isoform 4, isoform 6, isoform 7 and isoform 8).
/FTId=VSP_004246.
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Local Similarity 24.1%; Score 225.5; DB 1; Length 864;
Local Similarity 24.1%; Pred. No. 0.0004;
es 182; Conservative 59; Mismatches 271; Indels 242;
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Structural protein; Connective tissue; Repeat; Signal;
Alternative splicing.
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IsoId=099372-6; Sequence=VSP_004245, VSP_004246;
                                                                                                IsoId=Q99372-5; Sequence=VSP_004244, VSP_004245;
                                                                                                                                                      IsoId=099372-7; Sequence=VSP_004244, VSP_004246;
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Name=2;
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                                         IsoId=099372-3; Sequence=VSP_004245;
                                                                    IsoId=Q99372-4; Sequence=VSP_004246;
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EMBL, M86363, AAA42271.1, JOINED.
EMBL, M86364, AAA42271.1, JOINED.
EMBL, M86311, AAA42271.1, JOINED.
EMBL, M86311, AAA42271.1, JOINED.
EMBL, M86312, AAA42271.1, JOINED.
EMBL, M86373, AAA42272.1, JOINED.
EMBL, M86373, AAA42272.1, JOINED.
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InterPro; IPR003979; tropoelastin.
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AAA42271.1; -.
AAA42271.1; JOINED.
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                                                                                                                                 --GAGTLGGLVPG-----
122 SPAAAAKAAAK--YGARGGVGIPTYGVGAGGFPGYGVGAGAGL----
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Job time : 12.8689 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 30, 2004, 16:43:01; Search time 53.0977 Seconds (without alignments) 4331.879 Million cell updates/sec Run on:

Title: Perfect score:

US-09-597-796C-12 3686 1 MHHHHHHTAASDNFQLSQGG.....SGGPVVNGLGQVVGMNTAAS 729

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 segs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL 25:*
1: Sp archea:*
2: Sp bacteria:*
3: Sp fungi:*
4: Sp human:*
5: Sp invertebrate:*
6: Sp mammal:*
7: Sp mho:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	% Query				
Score		Match Length DB	DB	ΩI	Description
1944	52.7	391	16	005298	O05298 mycobacteri
20.5			16	Q7U0E9	Q7u0e9 mycobacteri
79.5			16	070071	Q7u071 mycobacteri
1648			16	OBVIZ3	Q8viz3 mycobacteri
1583			16	006341	006341 mycobacteri
1583			16	Q7TWF5	Q7twf5 mycobacteri
989			16	007175	007175 mycobacteri
989			16	Q7U2S9	Q7u2s9 mycobacteri
78.5			7	050320	Q50320 mycobacteri
75.5			16	Q7TZJ3	Q7tzj3 mycobacteri
75.5			16	053939	O53939 mycobacteri
758.5	20.6	410	7	099011	Q99qil mycobacteri
54.5			16	630CX9	Q9ccy9 mycobacteri
53.5			16	053957	O53957 mycobacteri
53.5			16	Q7TZH7	Q7tzh7 mycobacteri
737			16	053950	O53950 mycobacteri

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Q7TZI4	Q7TZH8	Q9Z5K0	053956	006386	P96362	Q7U0TS	QBVJWO	053958	P95190	97TX66	Q7TXX5	033310	Q7TZR7	033204	QBVJZ0	053940	Q7TZJ5	Q7TZJ2	086373	QBVJWS	Q7TX67	Q9AGF0	033312	Q8VKL9	Q7TXX3	Q7U242	Q7U114	005907
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737	736.5	734	733.5	700	697	69.7	969	689	674	674	671.5	670.5	667.5	664.5	663.5	641	641	637	633.5	633.5	628.5	616.5	615.5	615.5	613.5	609.5	605.5	605.5
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ALIGNMENTS

			cetales;				her C., Harris D.	ekala F.,	n N., Holroyd S.,	, Murphy L.,	Rogers U., is R.,		is from the),, Hickey E., D., Salzberg S.L.			is clinical and	ıses.
391 AA.	ed) seguence update)	ocación apasce/ stein).	Mycobacterium tuberculosis. Bacteria: Actinobacteria: Actinobacteridae: Actinomycetales	Corynebacterineae; Mycobacteriaceae; Mycobacterium. NCBI_TaxID=1773;			Parnier T., Churc	Gordon S.V., Eigimeler K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,	Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd	Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,	dandream M.A., Koyer nares S., Squares R.,	, Taylor K., Whitehead S., Barrell B.G.;	"Deciphering the biology of Mycobacterium tuberculosis complete genome sequence.":				Fleischmann R.D., Alland D., Eisen J.A., Carpenter L.,	Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeya M.D.	, Khouri H., Gil	•	Mycobacterium tuberculosis	EMBL/GenBank/DDBJ databases
PRT;		٦ ٢	sis.	pacteriaceae		1=9634230;	arkhill J., C	Srown D., Ch	eltwell T., ((rogh A., McI	relton S., So	Whitehead 8	/ of Mycobact			sh;	1 D., Eisen	odson R., G. I. Umavam L	, Weidman J		n of Mycobaci	
PRELIMINARY;	(TrEMBLrel. 04, Creat (TrEMBLrel. 04, Last	Ol-Oci-2003 (Iffinabliel: 23, Las Hypothetical protein (PPE famil: RV1196 OR MTCI364.08 OR MT1234.	Mycobacterium tuberculosis Bacteria: Actinobacteria;	rineae; Mycok 1773;	OM N.A.	v; 95987; PubMec	Cole S.T., Brosch R., Parkhill J.,	, Elgimeler r Basham D., I	Devlin K., Fe	Jagels K., I	Seeger K., S	., Taylor K.,	g the biology	Nature 393:537-544 (1998).	A N	STRAIN=CDC 1551 / Oshkosh;	R.D., Alland	, DeBoy R., I	Utterback T		"Whole genome comparison of	Laboratory strains."; Submitted (APR-2001) to the
UT 1 98 005298	01-JUL-1997 01-JUL-1997 01-JUL-1997	Hypothetical RV1196 OR MTC	Mycobactering Bacteria A	Corynebacterinea NCBI_TaxID=1773;	[1] SEQUENCE FROM N.A.	STRAIN=H37RV; MEDLINE=98295	Cole S.T.,	Gordon S.V. Badcock K.,	Davies R.,	Hornsby T.,	Rutter S.,	Sulston J.E.,	"Decipherin	Nature 393:	[2]	STRAIN=CDC	Fleischmann	Feterson J.	Delcher A.,	Bishai W.;	"Whole geno	Laboratory strains."; Submitted (APR-2001)
RESULT 005298 ID O	DT	SEC	88	888	R G	2 X	8	¥ ¥	Æ	Z:	¥ \$	\$	T T	Z.	Z 6	2	RA	RA PA	R.	RA	K 1	집

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STRAIN=AF2122/97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LIATNÍLÍGONTPAIAVNEAEÝGEMWAQDAAAMFGÝAAATATATATLLPFEEAPEMTSAGG 180
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                                                                                                                                                                                                                                                                                                                        142 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                 1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Dognett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. U.S. A. 100:7877-7882(2003).
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                                                                                                                                                                                                                                 Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                          Indels
                                                                                       Tuberculist, Rv1196; -.
InterPro, IPR000030; Microbac_PPE.
Pfam, PF00823; PEE, I.
Hypothetical protein; Complete proteome.
SEQUENCE 391 AA; 39158 MW; E409396B3ABDC0F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 AA; 39013 MW; 42788276BAB0B436 CRC64;
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Last annotation update)
                                                                                                                                                                                                                            52.7%; Score 1944; DB 16; 99.7%; Pred. No. 2.6e-85; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
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EMBL; Z93777; CAB07839.1; -.
EMBL; AZ007000; AAK45491.1;
PIR; B70608; B70608.
TIGR; MT1234; -.
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                          Conservative
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PPE18 OR MB1228.
                                                                                                                                                                                                                                                    Similarity
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STRAIN=AF2122/97;
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SEQUENCE 390 AA;
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Best Local Simi
Matches 390;
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SEQUENCE
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MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 201
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                                                       1 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                               SSAGLMYAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPVIAENRAELMI
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                                                                                                                 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                               LIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25,
01-0CT-2003 (TrEMBLrel. 25,
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Matches 364; Conservative
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GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLITSLTSAAERGPGQMLG 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98255987; PubMed=9634230; Garnier T., Churcher C., Harris I Gordon S.V., Eighmeier K., Gas S., Barry C.B. III. Tekaia F., Badcock K., Basham D., Erown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Taylor K., Whitehead S., Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Rv3478.
Rv3478 OR MTCX13E12.31.
Mycobacterium tubercullosis.
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium.
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393 AA; 39413 MW; AF4C20C95DAE7DD4 CRC64;
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                                                                                                                                                                                                                                 GLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           393
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InterPro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome sequence.";
Nature 393:537-544(1998).
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322; Conserv
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                                                                                                                                                                                                                                                                                                                      GSSGLGAGVAANLGRAASVGSLSVPPAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
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STRAINS-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alband D., Eisen J.A., Eaft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                            1 MVDFGALPPEINSARMYAGPGSASLVAAAKWWDSVASDLFSAASAFOSVVWGLTTGSWIG
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                                                                                                                                                                                                                                                         GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG
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; Pred. No. 3.5e-71;
20; Mismatches 34; Indels 6
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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|GLPLGQLTNSGGGFGGVSNALRMPRAYWMPRVPAAG 396
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PROSITE; PS00501; SPASE I 1; 1.
GEOTTENCE 393 AA; 39688 MW;
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Matches 335; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIEQAAAVEEASDIAAANQLMNNVPQALQQLAQPIQGTTPSSKLGGLWKTVSPHRSPISN 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSGLGGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 497
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Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 393;
                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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                                                                                                                                                  Last sequence update)
Last annotation update)
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81.5%; Pred. No. 4.4e-68;
tive 20; Mismatches 47;
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|GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
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|GDPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
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                                   GLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAG
                                                                                                                                       Created)
                                                                                                                   PRT;
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Best Local Similarity 81.5%
Matches 322; Conservative
                                                                                                                      OTTRES;
01-OCT-2003 (TERMBLES). 2:
01-OCT-2003 (TERMBLES). 2:
01-OCT-2003 (TERMBLES). 2:
PE family protein.
                                                                                                                  PRELIMINARY;
                                                                                                                                                                                               Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
SEQUENCE 393 AA;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=AF2122/97;
             300
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88 GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLFSAAIGGGV 147
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Fleischmann R.D.; Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D.; Alland D., Eisen J.A., Faft D., Hickey E.,
Fleterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonsy J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Cole S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III. Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.
Hiornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sliston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
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                                                                                                                                                       Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Hypothetical protein; Serine protease; Protease;
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SEOUENCE 355 AA; 34926 MW; 16CE9E21A97BF192 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; I
GO; GO:0006508; P:roteclysis and peptidolysis; IEA.
InterPro; IPR009403; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ.
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein (Serine protease, putative).
PEPA OR RV0125 OR MTC1418B.07 OR MT0133.
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InterPro; IPR008256; Peptidase S1B V8.
InterPro; IPR001940; Peptidase S1C.
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PROSITE; PS00135; TRYPSIN_SER; 1.
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EMBL; AE006925; AAK44357.1; -.
PIR; E70983; F70983
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Pfam; PF00189; trypsin; 1.
PRINTS; PR00189; PROTEASES2C.
PRINTS; PR001899; VBROTEASE.
SMART; SM00228; PDZ; 1.
                                                                                                                                   Mycobacterium tuberculosis.
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Tuberculist; R
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355 AA.

007175; 01-JUL-1997 (TrEMBLrel. 04, Created)

PRELIMINARY;

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60 SAWYGQYGPQVVNIDTKFGYNNAVGAGTGIVIDPNGVVLTNNHVISGATEISAFDVGNGQ 119
555 SAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22709107; PubNed=12788972; Medina N., Mansoor H., Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; EMBL; BX248340; CAD94520.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 VVALNĢSVSATDILIGAQENLGGLIQADAPIKPGDSGGPMVNSAGQVIGVDTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 361;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                  21.1%; Score 778.5; DB 2; Length 66.0%; Pred. No. 9.5e-30; ive 28; Mismatches 37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 30FEF78FD6F3C411 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                          Hydrolase, Protease, Serine protease, Signal. SIGNAL 1 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 155; Conservative
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SEQUENCE 393 AA:
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Matches 178;
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             148 AVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGD 207
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MEDLINE=22709107;
DELINE=2709107;
MEDLINE=2709107;
DELINE=2709107;
DELINE=2709107;
DELINE=2709107;
DELINE=2709107;
DELINE J. SIMONO S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkill J., Barrell B.G., Golles S.T., Gordon S.V., Hewinson R.G.;
The complete genome sequence of Mycobaccerium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
BMBL; BX248334; CAD92991.1;
BMBL; BX248334; CAD92991.1;
BHGUASS; Complete proceome.
SEQUENCE 355 AA; 34926 MW; 16CE9E21A97BF192 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=JDB8/107; STRAIN=JDB8/107; SPEDINE=95005449; PubMed=7921248; Cameron R.M., Stevenson K., Inglis N.F., Klausen J., Sharp J.M.; "Identification and characterisation of a putative serine protease
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
34KDa protein precursor.
Mycobacterium paratuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.8%; Score 989; DB 16; Length 355; 98.0%; Pred. No. 8.4e-40; ive 0; Mismatches 4; Indels
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Mycobacterium bovis.
Bacreria, Actinobacteria, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable serine protease PEPA (EC 3.4.21.-).
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                                                                                  SGGPVVNGLGQVVGMNTAAS 227
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Matches 196; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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01-NOV-1996
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Microbac_PPE

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InterPro; IPR000030; Mi
Pfam; PF00823; PPE; 1.
Tuberculist; Rv1789;
                                                                                                            Complete proteome.
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                                                                    IATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
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                                                                                                                                                                      SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delloher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Peltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Stuter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
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Submitted (ARR.2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17711.1; ALT_INIT.
EMBL; AE0070431; AAK46108.1; -.
PIR; G70929; G70929.
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RV1789 OR MT1838 OR MTV049.11.
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Nature 393:537-544(1998).
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PIR, G70929; G. J. TIGR; MT1838; -.

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                                                                                                                                                                      19 MDFGALPPEVNSVRNYAGPGSAPMVAAASAWNGLAAELSSAATGYETVITQLSSEGWLGP
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                                                Length 411;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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STRAIN=myc 94-2272, and 0V254;
SIVADN V., Heym B., Masznancurt P., Gaillard J.-L.L.;
Sivadon V., Heym B., Masznancurt P., Gaillard J.-L.L.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF335180; ARX20894:1;
InterPro; IPR000030; Microbac_PPE.
40557 MW; 03C90BSE0590B7DA CRC64;
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SEQUENCE 410 AA; 40044 MW; 3B9DA3174655A5EA CRC64;
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Last annotation update)
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43.4%; Pred. No. 1.6e-29;
ive 65; Mismatches 130;
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Q99Q11,
Q1-UTN-2001 (TERMBLEE) 1.
01-UTN-2001 (TERMBLEE) 1.
01-CTT-2002 (TERMBLEE) 2.
RV1808-like protein.
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  411 AA;
                                                                     Best Local Similarity
Matches 178; Conserv
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644 AIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEFTLNGLIQFDA
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Deloher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
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MEDLINE=98295987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris

Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Badcock K., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd Hornsby T., Jagels K., Krogh A., Micens S., Murphy L.,

Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                      Query Match
20.5%; Score 754.5; DB 16; Length 354;
Best Local Similarity 73.3%; Pred. No. 1.3e-28;
Matches 151; Conservative 25; Mismatches 25; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                  Hydrolase, Protease, Serine protease, Complete proteome. SEQUENCE 354 AA, 35265 MW, 612F23261BC9EA4A CRC64;
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01-UNN-1998 (TrEMBLrel. 06, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
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EMBL, AE007044; AAK46129.1; ALT_INIT.
PIR; A70932; A70932.
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InterPro; IPR000030; Microbac PPB.
Pfam; PF00823; PPE; 1.
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RV1808 OR MT1856.1 OR MTV049.30.
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   PROSITE; PS50106; PDZ; 1.
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COLE S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

COLE S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

Advise R.M., Devlin K., Duthop S., Feltwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Larcoix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Simon S., Stanon S., Stevens K., Simon S., Simmonds M., Skelton J., Squares R.,

Barrell B.G.; Are S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

"Massive gene decay in the leprosy bacillus.";

"Massive gene decay in the leprosy bacillus.";

"Mature 409:1007-1011(2001).

EMBL, ALS83956; CAC32191.1; -.

Parkens M. SALLA RANILY.
280 ILGPKAAAGALSPLAPLRGGYIADITPLGGGATGGIARAIYVGSLSVPQGWAEAAVWRA 339
                                                                                                                                                                                                                                                                                                                                                                                                   375 HRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAA------ARQAVQTAA 423
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                                                                                                           LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFCYAAATATATATLLPFEEAPEMTSAGG 321
                                                                                                                                                                                                                                                     322 ILEGAAAVEEASDTAAA-----NOLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSP 374
                                                                                                                                                                                                                                                                                               AARALPLTSLTSA-AERGPGQMLGGLPVGQMGARAGGGL----SGVLRVPPRPYVMPHS
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

GO; GO:0005298; P:proteolysis and peptidolysis; IEA.

InterPro; IPR009003; Cys_Ser_trypsin.

InterPro; IPR001249; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001896; Peptidase_S1C.

Pfam; PF00089; trypsin; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable secreted serine protease.
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PRINTS; PR00839; V8PROTEASE.
SMART; SM00228; PDZ; 1.
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                                                                                                               SAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 262
                                                                                                                                                                                                                              LEQAAAVEEASDTAAA-----NQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH 375
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                                                         VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                       IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
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                              Gaps
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MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
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Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
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Proc. Natl. Acad. Sci. U.S. A. 100:7877-7882(2003).
                              65;
   DB 16; Length 409;
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Bacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                              Indels
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Last annotation update)
Query Match 20.4%; Score 753.5; DB 16; Best Local Similarity 41.8%; Pred. No. 1.7e-28; Matches 184; Conservative 52; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.4%; Score 753.5; DB 16; 41.4%; Pred. No. 1.7e-28; ive 51; Mismatches 142;
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Matches 182; Conservative 5
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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PPE32 OR MB1837.
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SEQUENCE 409 AA;
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                                                                                                                                                61 SSITMAAAVAPYVAWISVTAGQAEQAGAQAKIAAGVYETAFAATVPPPVIEANRALLMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 LEQAAAVEEASDTAAA-----NQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAA------ARQAVQTAAQ
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SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
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Mycobacte Antigenic Mycobacte

Mýcobacte Mycobacte M. tuberc

M. tuberc Mycobacte M. tuberc M. tuberc Mycobacte Mycobacte Mycobacte Mycobacte

Protein e Protein e tuberc

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous bolynuclectide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynuclectide sequence encoding a polypeptide or its fragment. The Leishmania polynuclectide is selected from TSA, LeIF, MIS, and 6H polynuclectides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic
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Ra12; WTB72F; fusion protein.
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Aaw81702 N
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Aau01888
                                                                                                              Aaw32449
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                                                  Aau74597
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                                                                                    AAW32381
AAW32449
AAW32449
AAW81702
AAX39130
AAX39130
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ABU36968
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Mycobacterium tuberculosis.
Chimeric.
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   (revised)
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N-PSDB; AAD47083.
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27-JAN-2003
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(c) 1993 - 2004 Compugen Ltd.
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microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is MTB72F fusion protein. This fusion protein comprises Ral2 and Ra35 protein from M. tuberculosis and Th99 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to estandardise OS field)
                                                                                                                                                                                                                                                                                                                                NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120
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Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 729; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wycobacterium species antigons, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigons which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infeation or maintending and in the diagnosis, for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis of an infection or monitoring of disease progression, as immunosens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding Mycobacterium species MTB72F (Ra12-TbH9-Ra35) fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a subject
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to fusion proteins containing at least
                                                                            Fusion protein; antigen; serological sensitivity; immune response;
tuberculosis; infection; vaccine; MTB72F; Ra12-TDH9-Ra35 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in
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                                      Mycobacterium species MTB72F fusion protein.
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/label= TbH9FL_protein
                                                                                                                                                                                          8. .139
/label= Ra12_protein
                                                                                                                                                                                                                                                              535. .729
/label= Ra35_protein
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01-FEB-2001; 2001US-0265737P.
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Guderian J;

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WPI; 2001-266299/27
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e; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
                                                                                                     FSAASAFQSVVWGLTVGSWIGSSAGLWVAAASPVVAWMSVTAGQAELTAAQVRVAAAAYE
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                                                 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
                                                                                    FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE
                                                                                                                                                                                                                ATATATLI PFEEAPEMTSAGGLI EQAAAVEEASDTAAANQI MNNVPQALQQLAQPTQGTT
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tusion polypeptide, comprising a polymucleotide sequence of Ra12, a 14

Cusion polypeptide, comprising a polymucleotide sequence of Ra12, a 14

Cusion polypeptide, comprising a polymucleotide sequence of Ra12, a 14

Cusion for a cerminal fragment of serine protease artigen MTB32A of

Mycobacterium tuberculosis, and a heterologous polymucleotide sequence.

Cusion mucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cusion providing ratable and high yield expression of fusion polypeptides of both cusion and an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that cusion cources of proteins and as an immunogen to induce and/or enhance immune responses.

Cusion sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This sequence represents the Ra12-

H9-32A fusion protein
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                                                  Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
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Best Local Similarity 99.9%; Pred. No. 3.1e-233;
Matches 728; Conservative 0; Mismatches 1;
                                                                                                                                                                                         Disclosure, Fig 6, 39pp, English.
AAL40773
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NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120
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                                                                                                                                                                                                                                                                         361 PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQ
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                                        FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE
                                                                                                   TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT
                                                                                                                                                          TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEABYGEMWAQDAAMFGYAAAT
                                                                                                                                                                                                                                                                                                    TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP
                                                                                                                                                                                                                                                                                                                                                                                   LISLISAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS
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                                                                                                                                                                                                                                                                                                                      LISLISAAERGPGOMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS
                                                                                                                                                                                                                                                                                                                                                                                                                  QDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
                                                                                                                                                                                           ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT
                           TKSGGTRTGNVTLAEGPPAEFWVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion protein, MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium MTB72F-MTI (fusion MTB83F) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32A, MTB35A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has thereforestatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a polymucelotide of the invention may have a use in gene therapy, and as a polymucelotide of the invention to the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                   1 MHHHHHTAASDNEQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
                 GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN
                                 GATDINAFSVGSGOTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN
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                                                                     SGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQ
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                                                                                                                                                                                                                                                                                                                                  fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB35A; tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%; Score 3680; DB 7; Length 813; 99.9%; Pred. No. 3.6e-233; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                       Mycobacterium MTB72F-DPV (fusion MTB81F) protein.
                                                                                                                                                                                                                       AA.
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                                                                                                                                                                                                                       ADA26367 standard; protein; 813
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Matches 728; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB12A and MTB19 antigen, or MTB12A, MTB19 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a polymucelotide of the invention may have a use in gene therapy, and as a polymucelotide, and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120
661 SGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQ 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating
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                                                                                                                                                                                                                                                                                   fusion protein, MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 875;
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                                                                                                                                                                                                                                                     Mycobacterium MTB72F-Erd14 (fusion MTB89F) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 3680; DB 7;
Pred. No. 4e-233;
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Best Local Similarity
Lines 728; Conservative
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N-PSDB; ADA26358.
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                                                                                                                                                                                                 The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                  New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB55A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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N-PSDB; AAD47110.
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fusion polypeptide. The recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous computation prolypeptide sequence encoding an antigen or an antigenic fragment from CC Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, MI5, and 6H polymucleotides. Sequences of the invention CC are used in methods for eliciting immune response in mammals. They are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic CC microorganisms such as Leishmania and Mycobacterium tuberculosis. Pusion CC polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human CC minal. The invention is used in gene therapy. The present sequence is CMycobacterium spentism protein. This sequence comprises Mycobacterium species MTB72F (a 72 kDa poly-protein fusion construct comprising Ralz-CC TDH9-Rals) linked to the Leishmania TSA (MAPS). (Updated on 29-AUG-2003 CC TDH9-Rals) linked to the Leishmania TSA (MAPS). (Updated on 29-AUG-2003)
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New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
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Pred. No. 4.3e-233;
0; Mismatches 1;
                                                                                                            Example 6; Page 129-132; 155pp; English
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Best Local Similarity
Matches 728; Conserv
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GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN

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New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating

Disclosure; Fig 12; 112pp; English.

The invention relates to a novel nucleic acid encoding a fusion by Dypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB35 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypurclotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.

Sequence 930 AA;

Gaps .. 0 Score 3680; DB 7; Length 930; Pred. No. 4.3e-233; 0; Mismatches 1; Indels 99.8%; Matches 728; Conservative Query Match Best Local Similarity à

NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120 9 WHHHHHHHAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD 61

121 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL 180

61

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180 300 480 300 360 PSSKLGGLWKTVSPHRSPISNWVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQ 420 TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP 480 009 660 99 720 FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE 241 TAYGLTVPPVIAENRAELMILLATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANOLMNNVPOALOOLAOPTOGTT 421 TAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN 661 SGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQ LISLISAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS 541 QDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN SGGOGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQ 729 VVGMNTAAS VVGMNTAAS 361 181 181 361 301 301 121 601 481 601 661 721 721 ò qq 8 8 ઠે 셤 q d d ઠે ò ò ઠે 엄 à 셤 8 g à

Ą protein; 1016 ADA26370 standard;

(first entry) 20-NOV-2003 ADA26370;

M. bovis MTB72F and 85b complex antigen (fusion MTB103F).

fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine; MTB72F; 85B

Mycobacterium bovis, Chimeric.

402003070187-A2.

38-AUG-2003

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18-FEB-2003; 2003WO-US004903

LS-FEB-2002; 2002US-0357351P.

(CORI-) CORIXA CORP

Reed S; Guderian J, Skeiky Y,

WPI; 2003-697554/66

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                                                                                                   The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or WTB32A, WTB32A and MTB39 antigen, from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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a fusion polypeptide with the MTB32A the MTB85A antigen, from a
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                                                                                                                                                                                                                                                                                                      Gaps
   New isolated nucleic acid encoding a fusion polypeptide with the and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or
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                                                                                                                                                                                                                                                                      Score 3680; DB 7;
Pred. No. 4.8e-233;
0; Mismatches 1;
                                                                            English
                                                                                                                                                                                                                                                                           99.8%;
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.9
Matches 728; Conservative
                                                                              Claim 85; Fig 18; 112pp;
                                                 tuberculosis infection.
                                                                                                                                                                                                                                                Sequence 1016 AA;
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or WTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymelotide of the invention may have a use in gene therapy, and as a polymer. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                                                                                                                                                                                                                                                                      fusion protein, MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
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                                                                                                                                                                                                                                                                                 Mycobacterium MTB72F-hTCC#1 (fusion MTB102tm2F) protein.
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Pred. No. 4.8e-233;
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                                                                                                                             standard; protein; 1022 AA.
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Best Local Similarity 99.9
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VVGMINTAAS
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Claim 85; Fig 16; 112pp; English.
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                                                                                 PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQ
                                                                                                                                                                                                                                                                 SGGGGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQ
TAYGLTVPPPVIAENRAELMILLATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAAT
                                              ATATATLIPFEBAPEMTSAGGLIEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT
                                                                                                                                                       ODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
          TAYGLTVPPPVIAENRAELMILIATNILGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT
                                   ATATATLL PFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT
                                                                      PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQ
                                                                                                         TAAQNGVRAMSSLGSSLGSSGLGGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP
                                                                                                                          421 TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP
                                                                                                                                             LISLISAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS
                                                                                                                                                                               QDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
                                                                                                                                                                                                                   GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN
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                                                                                                                                                                                                                                                     SGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                            fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A; tuberculosis; tuberculosis; tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium MTB72F-mTCC#2 (fusion MTB114F) protein.
                                                                                                                                                                                                                                                                                                                                                      protein; 1154 AA
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB12A and MTB19 antigen, or MTB12A, MTB19 and MTB18A and mtrgen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymerolotide of the invention may have a use in gene therapy, and as a yecine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE
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                                                   TAYGETVPPPVIAENRAELMILIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGXAAAT
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                                                                                                                                                                                                                                                                                                                   481 LTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS
                                                                                                                                                                                                                                                                                                                                                                                                                    GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; antigen; serological sensitivity; immune response;
tuberculosis; infection; vaccine; MTB72FMutSA; Ra12-TDH9-Ra35MutSA,
mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild type Ser substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium species MTB72FMutSA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142. .532
|Tabel= TbH9FL_protein
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/label= Ra12_protein
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/label= Ra35_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE17573 standard; protein; 729 AA.
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01-FEB-2001; 2001US-0265737P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polypuclectide sequence encoding an antigen or an antigenic fragment from polypeptide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polymucleotide sequence encoding a polypeptide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, MIS, and 6H polymucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is mimal. The invention protein fusion protein and Ral2 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      new recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKSGGTRIGNVTLAEGPPAEFWVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
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                                                                                                                               Vaccine, immunity, diagnostic agent, gene therapy, TbH9, antigen,
Ra35MutSA, Ra12, MTB72MutSA, fusion protein.
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Best Local Similarity 99.7%; Pred. No. 5e-233;
Matches 727; Conservative 1; Mismatches 1;
                                                                                                Mycobacterium sp. MTB72FMutSA fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 93-95; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Guderian J;
                                                                                                                                                                                                                                                                                                         13-MAR-2002; 2002WO-US008223.
                                                                                                                                                                                                                                                                                                                                          13-MAR-2001; 2001US-0275837P.
                                                                                                                                                                             Mycobacterium sp.
Mycobacterium tuberculosis.
                                                                  (first entry)
                                                   (revised)
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                                               29-AUG-2003
27-JAN-2003
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                 AAE29709;
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with increase the exploration and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatments of with EGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymorlectides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WTB32A full intradermal skin test. The present sequence is Mycobacterium species mTB72FMutSA (Ral2-TbH9-Ra35WutSA) mutant fusion protein
                                                                                                                                                                                                                                                                                                                                                           Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 88; Fig 5; 136pp; English.
                                                                                                   Reed S, Alderson M;
CORIXA CORP.
                                                                                                                                                                                                            2002-147798/19
                                                                                                                                                                                                            WPI; 2002-147798,
N-PSDB; AAD28343
                                                                                                        Skeiky Y,
     (CORI-)
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Sequence 729 AA;

420 120 61 NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ 120 180 180 240 TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT 300 300 360 420 FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE 240 301 ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMINVPQALQQLAQPTQGTT 360 9 9 1 MIHHHHHTAASDNFQLSQGGQFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAMRGYAAAT NNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQ TKSGGTRTGNVTLAEGPPAEFWVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL 121 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL ATATALLIPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQ 361 PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQ MHHHHHHAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD ö 99.8%; Score 3677; DB 5; Length 729; 99.7%; Pred. No. 5e-233; ive 1; Mismatches 1; Indels 727; Conservative Best Local Similarity 181 -361 61 121 181 241 241 301 Query Match Matches g à g à 엄 ð d ö g $\dot{\delta}$ 면 ò g à

Sequence 729 AA;

480 480

TAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALP

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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB99 antigen, or MTB32A, MTB99 and MTB95A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polynucelotide of the invention may have a use in gene therapy, and as a vaccine. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating
                                                                                                                                                                       661 SGGQGGTPRAVPGRVVALGQTVQASDSLTGAEFTLNGLIQFDAAIQPGDAGGPVVNGLGQ
               GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN
                                                     ODRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIA
                                                                                                      GATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN
LISLISAAERGPGOMLGGLPVGOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALS
                                                                                                                                                                                                                                                                                                                                                                                                              MTB32A; MTB39; antigen; MTB32A; MTB39; WTB85A; tuberculosis;
tuberculostatic; gene therapy; vaccine; WTB72F; mutant; mutein.
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Misc-difference 710
/note= "Wild-type Ser substituted by
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                                                                                                           MHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTALGLGVVD
                                                                                                                                                                                                                                      TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
                                                                                                                                                                                                                                                                                                                                         FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE
                                                                                                                                                                                                                                                                                                                                                                                                                      ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTT
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                                                                                MHHHHHTAASDNFQLSQGGGGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVVD
                                                                                                                                                                                                                                                                       121 TKSGGTRTGNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDL
                                                                                                                                                                                                                                                                                                                     FSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYE
                                                                                                                                                                                                                                                                                                                                                                                               TAYGLTVPPPVIAENRAELMILIATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATATATLLPFEEAPEMTSAGGLLEQAAAVEEASDTAAANQLMNVVPQALQQLAQPTQGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSSKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAARQAVQ
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                                             ;
    7; Length 729
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  Score 3677; DB 7
Pred. No. 5e-233;
1; Mismatches
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Query Match
Best Local Similarity 99.7
Matches 727; Conservative
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB12A and MTB13 antigen, or MTB12A, MTB13A and MTB15A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a use in gene therapy, and as a polynucelotide of the invention for the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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Pred. No. 1.4e-232;
0; Mismatches 2;
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                                                  18-FEB-2003; 2003WO-US004903
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Best Local Similarity 99.7
Matches 727; Conservative
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Scoring table:

1017041 seqs, 315518202 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1017041 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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sp_organelle:*
sp_organel sp_rvirus:*
sp_bacteriap:*
sp_archeap:* SPTREMBL 25:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

T 1 005298 PRELIMINARY; PRT; 391 AA. 005298;
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PPE family protein.
PPE19 OR MB1396C.
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MEDLINE=22709107; PubMed=12788972;
Garniaer T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garniaer T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Phyco. Natl. Acad. Sci. US.A. 100:7877-7882(2003).
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Best Local Similarity 99.0%; Pred. No. 9.6e-89;
Matches 387; Conservative 2; Mismatches 1; Indels 1;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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                                                                                                                                                    I protein; Complete proteome.
391 AA; 39158 MW; E409396B3ABDC0F8 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                 Query Match 64.8%; Score 1949; DB 16; Best Local Similarity 100.0%; Pred. No. 3.6e-90; Matches 391; Conservative 0; Mismatches 0;
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                                                                                   Tuberculist; Rv1196; -.
InterPro; IPR000030; Microbac PPE.
Pfam; PF00823; PPE; 1.
EMBL; 293777; CAB07839.1; -. EMBL; AE007000; AAK45491.1; PIR; B70608; B70608. TIGR; MT1234; -.
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SEQUENCE FROM N.A.
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                                 LIATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
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  MYDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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MEDLINE-22709107; PubMed-12788972;

MEDLINE-22709107; PubMed-12788972;

MEDLINE-22709107; PubMed-12788972;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

"The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. US.A. 100:7877-7882(2003).
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Matches 364; Conservative
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241 IVSMINNHVSMTNSGVSMASTLHSMLKGFAP-AAAQAVETAAZNGVQAMSSLGSQLGSSL 299
                                                                 GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLISLTSAAERGPGOMLG 364
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                                                                                       10 GSSGLGAGVAANLGRAASVGSLSVPQAWAANQAVTPAARALPLTSLTSAAQTAPGHMLG
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Rajandream M.A., Rogers J., Rutter S., Seeger K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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Last annotation update)
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                                                                                                                                                  365 GLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                            360 GLPLGH-SVNAGSGINNALRVPARAYAIPRIPAAG 393
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81.5%; Pred. No. 7.8e-72;
live 20; Mismatches 47
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PIR; C70568; C70568.
Tuberculist; Rv3478; -.
Interpro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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Matches 322; Conservative
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        006341;
01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
        248
                               LIEGAAAVEEASDTAAANOLMANVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHLSPISN 240
                                                                                         304
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                                                                                                                                                                            GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 364
                                                                                                                                                                                                       300 GSSGLGAGVAANLGRAASVGSLSVPPAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland B., Gwinn M.L., Haft D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                       LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                         MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSS----LGSSL
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AE007161; ARK47941.1; -..
GO, GO:0016020; -..
GO, GO:0016020; C:membrane; IEA.
GO, GO:0008233; F:peptidase activity; IEA.
GO, GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000030; Microbac PPE.
InterPro; IPR000509; Peptidase_S26.
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393 AA; 39688 MW; 86F0B67798855511 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                      GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 399
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84.8%; Pred. No. 4.3e-75;
iive 20; Mismatches 34
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01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
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PROSITE; PS00501; SPAS
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300 GSSGLGAGVAANLGRAASVGSLSVPPAWAAANQAVTPAARALPLISLISAAQTAPGHMLG 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
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                                                                                                                                                                                                                                                                                                                                  Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Color S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis.", Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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81.5%; Pred. No. 7.8e-72;
iive 20; Mismatches 47; Indels 6;
                                                                                                                                                                                                                              Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                             393 AA; 39413 MW; AF4C20C95DAE7DD4 CRC64;
                                                                                                                                                                           Last sequence update)
Last annotation update)
                                         365 GLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
                                                        360 GLPLGH-SVNAGSGINNALRVPARAYAIPRTPAAG 393
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                                                                                                                                     393 AA
                                                                                                                                                              Created)
                                                                                                                                     PRT;
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MEDLINE=22709107; Pubmed=12788972;
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EMBL, BX248346; CAD95692.1; -.
Complete proteome.
SEQUENCE 393 AA; 39413 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 81.5%
les 322; Conservative
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                   PE family protein. PPE60 OR MB3505.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDITRE=9825987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Biglameier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517 AVGEDVVAMGNSGQGGGTPRAVPGRVVALGGIVQASDSLIGAEETLNGLIQFDAAIQPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 AAGDIAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishai W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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PROSITE; PS00135; TRYPSIN SER; 1.
PAYORIDASE; Hypothetical protein; Serine protease; Protease; Complete proteons 34926 MW; 16CB9E21A97BF192 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMEL; AEOOGES; AAK44357.1; -.

PIRI; AEOOGES; AAK44357.1; -.

TIGR; MTO13; -.

TIGR; MTO13; -.

TOPECULIST; RV0125; -.

TOPECULIST; RV0125; -.

GO; GO:00004295; P:intracellular signaling cascade; IEA.

GO; GO:0000742; P:intracellular signaling cascade; IEA.

GO; GO:0000589; P:intracellular signaling cascade; IEA.

GO; GO:0000589; P:intracellular signaling cascade; IEA.

GO; GO:0000589; P:intracellular signaling cascade; IEA.

InterPro; IPR001249; PDZ; --

InterPro; IPR001249; Peptidase_S1.

InterPro; IPR001940; Peptidase_S1C.

PEam; PF00089; LYypsin; 1.

PEam; PF00089; LYypsin; 1.

PEAM; PR00089; PROTEASES.C.

PRINTS; PR00389; VBPROTEASES.C.

PRINTS; PR00289; PDZ; 1.
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
1-JUL-2003 (TrEMBLrel. 25, Last amnotation update)
Hypothetical protein (Serine protease, putative).
PEPA OR RV0125 OR MTC1418B.07 OR MT0133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z96071; CAB09453.1; -.
                                                                                                                                                     Mycobacterium tuberculosis.
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STRAIN-CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence.'
Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                NCBI_TaxID=1773;
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007175 PRELIMINARY; PRT; 007175; 01-JUL-1997 (TrEMBLrel. 04, Created)

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180 GTQAAAVATAAGTAQSTLTEMITGLPNALQSLTSPLLQSS-NGPLSWLWQILFGTPNFPT 238
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                                                                                                                                                                                                                                                                                                                                                                         70 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 GDAAKGLPGLGGMLG----GGPVAAGLGNAASVGKLSVPPVWSGPLPGSVTPGAAPLPVS
                                                                                                                                                                                                                                                                                                                                           10 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 LEQAAAVEEASDTAAA--NOLMNNVPQALQQLAQPTQGTTPSSKLGGLWK------
  Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "I'the complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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Oclo S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Teksia F. Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies K., Devlin K., Relwell T., Gentles S., Hamin N., Holrcyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Stegler K., Skellen S., Squares S., Squares R., Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLTSAAERGPGOMLGGLPVGOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 TVSAAPEAAPGSLLGGLPL----AGAGGAGAGP-RYGFRPTVMARPPFAG 393
                                                                                                                                                                                                                                           Length 393;
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                                                                                                                                                                                                                                      25.9%; Score 779.5; DB 16; Length 43.7%; Pred. No. 1.4e-31; ive 65; Mismatches 129; Indels
                                                                                                                                                                                       393 AA; 38572 MW; 41944B6E547A8AB0 CRC64;
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Last sequence update)
Last annotation update)
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RV1789 OR MT1838 OR MTV049.11.
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                 Best Local Similarity 43.7
Matches 179; Conservative
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                                                                                                                                                                 proteome
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                                                                                                                                                              Complete | SEQUENCE
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                                                                                                                                                                                                                                        Query Match
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148 AVGEPVVAMGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGD 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-AF2122/97;
MEDLINE-22709107;
MEDLINE-2709107;
PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase, Complete proteome.
SEQUENCE 355 AA; 34926 MW; 16CE9E21A97BF192 CRC64;
                                                                                                                                                                                                                                                                                  01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable serine protease PEPA (EC 3.4,21.-).
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Last annotation update)
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                                                                                                                                                                                                                                      355 AA
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                                                                                       208 SGGPVVNGLGQVVGMNTAAS 227
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                                                 SGGPVVNGLGQVVGMNTAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 98.0
Matches 196, Conservative
                                                                                                                                                                                                                        PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium bovis.
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PPE26 OR MB1817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1765;
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                                                                                                                                                                                                                                                                                                                                                                                          PEPA OR MB0130
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Q7U2S9;
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                                                                                                                                                                         RESULT 8
2070289
1D 2010-20
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DT 01-00
DE PEOD BECCOOC BECCOOC BECCOOC BECCOOC BECCOOC BECCOOC BECCOOC BECCOOC BECCOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BECOOC BE
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Gaps

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Best Local Similarity 66.0%
Matches 155; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium microti
                                                                                                                                                                                               Hydrolase; Protease;
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Q99QI1;
                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                       189
                                                                                                                                                                                                                                                                                                                                                                                                                                    198 GTQAAAVATAAGTAQSTLTEMITGLPNALQSLTSPLLQSS-NGPLSWLWQILFGTPNFPT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 QNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAA-ANQAVTPAARALPLT 349
                                                                                                                                                                                                                                                                                                           69
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                                                                                                                                                                                                                                                                                                         10 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                            311 GDAAKGLPGLGGMLG----GGPVAAGLGNAASVGKLSVPPVWSGPLPGSVTPGAAPLPVS
                                                                                                                                                                                                                                                                                                                                                                              130 IATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 SISALLTDLOPYASFFYNTEGLPYFSIGMGNNFIQSAKTL-GLIGSAAPAVA----AA
                                                                                                                                                                                                                                                                                 37; Gaps
Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A., Bishai W.;
                                                                      Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=JD88/107;

BDDLINE=95005449; PubMed=7921248;

Cameron R.M., Stevenson K., Inglis N.F., Klausen J., Sharp J.M.;

Cameron R.M., Stevenson K., Inglis N.F., Klausen J., Sharp J.M.;

Identification and characterisation of a putative serine protease

The stressed in vivo by Mycobacterium avium subsp paratuberculosis.";

Microbiology 140:1977-1988(1994).

-- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 LEQAAAVEEASDIAAA--NQLMNNVPQALQQLAQPTQGTTPSSKLGGLWK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 SLISAAERGPGOMLGGLPVGOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 TVSAAPEAAPGSLLGGLPL----AGAGGAGAGP-RYGFRPTVWARPPFAG 411
                                                                                                                                                                                                                                                        DB 16; Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34KDa protein precursor.
Mycobacterium paratuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                   / Match 25.9%; Score 779.5; DB 16; Length Local Similarity 43.7%; Pred. No. 1.5e-31; nes 179; Conservative 65; Mismatches 129; Indels
                                                                                         laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022021; CAA17711.1; ALT_INIT.
EMBL; AE007043; AAK46108.1; -.
                                                                                                                                                                                                                           03C90B5E0590B7DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AA
                                                                                                                                                                   Tuberculist; RV1789; -.
InterPro, IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                               40557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z23092; CAA80638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                             PIR; G70929; G70929.
TIGR; MT1838; -.
                                                                                                                                                                                                                                411 AA;
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                                                                                                                                                                                                                  Complete proteome
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                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 SAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 SAWVGQVGPQVVNIDITKFCYNNAVGAGTGIVIDPNGVVLTNNHVISGATEISAFDVGNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                               362. MIGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542 VVALGQTVQASDSLTGAEETLNGLLQFDAALQPGDSGGPVVNGLGQVVGMNTAAS 596
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                                                                                                                                                                                                                                                                                                                                                                 Length 361;
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NCBI_TaxID=1806;
GO; GO:000823; F: Peptidase activity; IEA.
GO; GO:000823; F: Prypsin activity; IEA.
GO; GO:0007242; P: Intracellular signaling cascade; IEA.
GO; GO:0006509; P: Proteolysis and peptidolysis; IEA.
InterPro; IPR00134; Peptidase_SI.
InterPro; IPR00134; Peptidase_SI.
InterPro; IPR00134; Peptidase_SI.
Feam; PF00595; PDZ; 1.
FEAM; PF00595; PDZ; 1.
FRAM; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
FROSITE; PS50106; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                        SEQUENCE 361 AA; 35709 MW; 30FEF78FD6F3C411 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.2%; Score 756.5; DB 2;
ilarity 42.4%; Pred. No. 2.1e-30;
Conservative 52; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                 25.9%; Score 778.5; DB 2; 66.0%; Pred. No. 1.4e-31; ive 28; Mismatches 37;
                                                                                                                                                                                                                                                              DZ; 1.; Serine protease; Signal. 38 POTENTIAL.
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STRAIN=myc 94-2272, and OV254;
Sivadon V., Heym B., Mazancourt
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PROSITE; PS50106; PDZ; 1.
Hydrolase; Protease; Serine protease; Complete proteome.
SEQUENCE 354 AA; 35265 MW; 612F23261BC9EA4A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 PIKPGDSGGPVVNSRGQVVGMNTAAT 227
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EMBL, AE007044; AAK46129.1; ALT_INIT.
PIR, A70932; A70932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 AIQPGDSGGPVVNGLGQVVGMNTAAS
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InterPro; IPR000030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
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Fleischmann R.D., Alland D.
                                                                                                                                       Similarity 73.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 393:537-544 (1998).
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O53957;
01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
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                                                                                                                                                                     151;
                                                                                                                   Query Match
                                                                                                                                                Local
                                                                                                                                                                        Matches
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241
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                                                                                                                      299 SLGSSLGS----SGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTS 353
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=9829597; PubMed=9634230;
Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holrcyd S.
Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L.,
Oliver S., Seeger K., Skelton S., Squares S., Squares R.,
Sultcon J.B., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
   16; Length
25.1%; Score 754.5; DB 16; Length
73.3%; Pred. No. 2.2e-30;
tive 25; Mismatches 25; Indels
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PPE-family protein.
RV1808 OR MI1856.1 OR MTV049.30.
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EMBL; BX248340; CAD94540.1; -. Complete proteome.

SEQUENCE 409 AA, 39931 MW, D57892628B131A9E CRC64;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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42.6%; Pred. No. 2.9e-30;
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01-0CT-2003 (TrEMBLrel. 25,
01-0CT-2003 (TrEMBLrel. 25,
Query Match
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PPE32 OR MB1837.
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                                                                        SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
               130 IATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLIPFEEAPEMTSAGGL
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OM protein - protein search, using sw model

June 30, 2004, 16:42:21; Search time 9.70351 Seconds (without alignments) 3198.204 Million cell updates/sec Run on:

US-09-597-796C-10 3007 1 HMHHHHHHWUDFGALPPEIN.....SGGFVVNGLGQVVGWNTAAS 596 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_42:* Database:

	Description	mycobacter	mycobact	mycobacter			mycobact			mycobacter		bacillus	mycobacte	arabidopsi	P31137 escherichia	chlamydia	homo sapi	022609 arabidopsis	escherich	Q9jiy5 mus musculu	baci	brucella	bacillu	buchnera		haemophil		н	brucella	P26982 salmonella	escheric	chlamydia	085291 buchnera ap	æ	
SUMMARIES		YD61 MYCTU	ö	20	YF48 MYCTU	\sim	Y878_MYCTU	SRA MYCLE	YU18 MYCTU	Y096 MYCTU	YU21 MYCTU	YVTA_BACSU	1	DEG8 ARATH	DEGS_ECOLI	DEGP_CHLPN	HRA2 HUMAN	DEG1_ARATH	DEGO_ECOLI	HRA2 MOUSE	HTRA_BACSU	DEGP_BRUSU	YYXA BACSU	DEGP_BUCAI	YY25 MYCTU	HTOA HABIN	HTRA_LACHE	DEGP_RICCN	DEGP_BRUME		DEGP_ECOLI		DEGP BUCAP	DEGP_CHLMU	
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)52894 rhizobium m)05942 rickettsia	P54925 bartonella Q99372 rattus norv P83105 homo sapien	15502 homo sapien 91a06 lactococcus	92743 homo sapien	9r118 mus musculu 83110 homo sapien	44947 haemophilus
90	F 0 F	2.0	O A G	2, 2	Д.
DEGP_RHIME DEGP_RICPR	DEGP_BARHE ELS_RAT HRA4 HUMAN	els Human HTRA_LACLA	HRAI HUMAN ELS BOVIN	HRAI MOUSE HRA3 HUMAN	DEGS_HAEIN
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3.4 3.5	36 37 38	39 40	441	4 4 6 4	45

ALIGNMENTS

RESULT YD61_M	RESULT 1 YD61 MYCTU TD YD61 MYCTU	STANDARD.	ркт.	44 A94	
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DŢ	01-OCT-1996 (F	tel. 34, Created	_		
DI	01-OCT-1996 (R	01-OCT-1996 (Rel. 34, Last seque	sequence update)	ipdate)	
텀	10-0CT-2003 (F	lel. 42, Last am	notation	annotation update)	
DE	Hypothetical F	PE-family prote:	in Rv136	1c/MT14(96.
S.	RV1361C OR MTI	RV1361C OR MT1406 OR MTCY02B10.25C.).25C.		
SO	Mycobacterium tuberculosis.	tuberculosis.			
ဗ	Bacteria, Acti	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales	inobacte	ridae; /	Actinomycetales;
ဗ	Corynebacterin	Corynebacterineae; Mycobacteriaceae; Mycobacterium.	aceae;	Mycobact	cerium.
ŏ	NCBI_TaxID=1773;	73;			
KN	[1]				
54 J	SEQUENCE FROM N.A	N.A.			
N N	STRAIN=H37RV;	•			
ĸ	MEDLINE=982959	987; PubMed=96342	230;		
R.	Cole S.T., Brc	sch R., Parkhill	L J., Ga	rnier T	., Churcher C., Harris D.,
RA	Gordon S.V., E	liglmeier K., Gae	3 S., Ba	rry C.E.	. III, Tekaia F.,
RA	Badcock K., Ba	sham D., Brown I)., Chil	lingwort	th T., Connor R.,
RA	Davies R., Dev	/lin K., Feltwell	T., Ge	ntles S	., Hamlin N., Holroyd S.,
RA	Hornsby T., Ja	iqels K., Kroqh A	A., McLe	an J., 1	
RA	Oliver S., Osb	orne J., Ouail N	f.A. Ra	jandrear	Oliver S., Osborne J., Onail M.A., Rajandream M.A., Roders J.
A A	Rutter S See	Ger K Skelton	ď	מקדות	Salaren R
A A	Sulston I E	Sulaton I E Havlor & Whitehead & Barrell B G.	יים לי המלי	1000	
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E C	Tomor of of the control of the contr	of company of m	CODACLO	1	
2 2	comptere genome sequence.	e seduence;			
R.	Nature 393:537	7-544(1998).			
KN	[2]				
RP	SEQUENCE FROM	N.A.			
RC	STRAIN=CDC 155	1 / Oshkosh;			
χX	MEDLINE=222064	94; PubMed=12218	3036;		
RA	Fleischmann R.	D., Alland D.	lisen J.	A. Carr	penter L. White O.
RA A	Peterson T. D	PEROV P Dodgon	2	× 11	Laft D Hickey E
P P	Volones T P	Nolock to the	The state of the s		Lance D., Interney D.,
5 ;	holollay U.F.,	NETSOIL M.C., OILIE	ayam n.s		ideva m., saizberg s.b.,
Ş	Delcher A., Ut	Terback I., Welc	man J.,	Khouri	H., Gill J., Mikula A.,
KA	Bishai W., Jac	obs W.R. Jr., Ve	enter J.	C., Fras	ser C.M.;
RT	"Whole-genome	comparison of My	rcobacte	rium tuk	perculosis clinical and
RT	laboratory str	ains.";			
RL	J. Bacteriol.	184:5479-5490(20	02).		
g	-!- SIMILARITY	: Belongs to the	mycoba	cterial	PPE family.
ပ္ပ					
ပ္ပ	This SWISS-PRO	T entry is copyr	right. I	t is pro	oduced through a collaboration
ខ្ល	between the S	wiss Institute o	of Bioin	formatic	s and the EMBL outstation -
g	the European B	Nioinformatics Ir	nstitute	. There	are no restrictions on its
g	use by non-p	profit instituti	ons as	long as	sits content is in no way
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A Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

T "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                    1 MVDFGALPPEINSARMYAGPGSASLVAAARMWDSVASDLFSAASAFQSVVWGLTTGSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                           241 IVSMLNNHVSMTNSGVSMASTLHSMLKGFAP-AAAQAVETAAQNGVQAMSSLGSQLGSSL
                                                                                                                                                                                                                                                                                                     SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                 61 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                           7,
                                                                                                                 55.1%; Score 1656.5; DB 1; Length 396; 85.1%; Pred. No. 5.5e-77; ive 18; Mismatches 34; Indels 7;
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NCBI_TaxID=1773, 1765;
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15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv2892c/MI2959/Mb2916c.
RV2892C OR MI2959 OR MICK274.23C OR MB2916C.
Mycobacterium tuberculosis, and
                                                   A -> AT (IN REF. 2).
6AFAE0D7B5F668D0 CRC64;
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    Pfam; PF00823; PPE; 1.
Hypothetical protein; Complete proteome.
CONFLICT 158 159 TA -> AT (1
                                                                       396 AA; 40015 MW;
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                                                                                                                                               Local Similarity
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SPECIES=M.tubercul
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                                                   CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 LEQAAA-----VEEASDTAAANQLMNN-----VP--QALQQ-LAQPTQGTTPSSKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GGLWKTVSPHRSPISNWVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAA
                                                                                                                                                                                                                                                  SPECIES—M. Dovis; STRAIN=AF2122/97; Medina N., Mansoor H., Garnier T., Eiglmeier K., Caums J.-C., Medina N., Mansoor H., Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. US. A. 100:7877-7882 (2003).
Ermolaeva M., Salzberg S.L., touri H., Gill J., Mikula A.,
      Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R., Jr., Venter J.C., Fraser C.M.; "Mole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 5.2e-29;
47; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculist; RV2892c; -.
InterPro; IPR000030; Microbac_PPE.
Pfam, PF00823; PPE; 1.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 56
POFENTIAL.
SSQUENCE 408 AA; 41469 MW; 3E3D1F20D7827199 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.4%; Score 705; DB 1;
41.8%; Pred. No. 5.2e-29;
                                                                                                                                                             Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE007119; AAK47285.1; -.
EMBL; BX248344; CAD96603.1; -.
PIR; G70925; G70925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z74024; CAA98377.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuberculist; Rv2892c;
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69 59

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SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 -SALGAGLGLRSAISSGLGSTAPAISAGASQAGSVGGMSVPPSWAAATPAIRTVAAVFSS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 MSSLGSSLG----SSGLGG---GVAANLGRAASVGSLSVPQAWAANQAVTPAARALPL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 ATQGVAVAQAVGASAGN-ARSLVSEVLEFLA--TAGTNYNKTVASLMNAVTGVPYASSVY
                                                                                                                                                                                             130 IATNILGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                     120 AATNIFGONTGALAABARYAEMWAQDAAAMYGYAGSSSVAT-QVTPFAAPPPTTNAAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 LEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS--PHRSPI-
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MEDLINES-9825987; PubMed=9634230;
MEDLINES-9825987; PubMed=9634230;
MEDLINES-9825987; PubMed=9634230;
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Earry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Krogh A., McLean J., Moule S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J.,
Rutter S., Osborne J., Selton S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Mature 393:537-544(1998).
                                                                                                                                                                10 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 NSMLGLGFAESKAVLPANDTVISTIFGMVQFQKFFNPVTPPNPDLIPK------
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MEDLINE=2220644; PubMed=1218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Eatt D., Hickey E.,
Kolonay J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                              Gaps
                                                                                                           49;
                                                       463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSLTS--AAERGPGQML-----GGLPVGQMGARAGGGLSGVLRV 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterinae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rgigavpaaisegsilsomalasvaggalggaaararggflgggrv 389
                                                    22.9%; Score 688.5; DB 1; Length 42.8%; Pred. No. 4e-28; ive 48; Mismatches 136; Indels
463 AA; 46021 MW; EE64828BF09FA551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0c7-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-0c7-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1548c/MT1599
RV1548C OR MT1599 OR MTCY48.17.
                                                                                                              Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                              Similarity
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  SEQUENCE
                                                    Query Match
Best Local S
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Q10778;
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YF48 MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIZER CHILDER STRAIN=H37Rv;
MEDIZER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER CHILDER 
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Ginn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Veneer J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains.";
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SPECIES=M. bovis; STRAIN=AF2122/97;
MEDLINE=22709107; bubMed=12788972;
MEDLINE=2709107; bubMed=12788972;
MEDLINE=2709107; bubMed=12788972;
Medina T., Eiglimeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrall B.G., Colle S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
-!- SIMILARITY: Belongs to the mycobacterial PPB family.
                                                                                                                                                                                                                                                                                                                                                    Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae; Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                     YI02_MYCTU STANDARD; PRT; 463 AA.
053951;
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
11-CCT-2013 (Rel. 42, Last annotation update)
12-CT-2013 (Rel. 42, Last annotation update)
13-CT-2013 (PREl. 42, Last annotation update)
14-YPOCHEGIA PPE family protein RV1802/MT1851/MD1830.
RV1802 OR MT1851 OR MTV049.24 OR MB1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculist; Rv1802; -.
InterPro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPE; 1.
Hypothetical protein, Complete proteome.
CONFLICT 401 401 S -> L (IN REF. 2).
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                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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TIGR; MT1851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 NLGGGNTGDLNPDSGNTGTLN----WGSGN------IGSYNLGGGN-LGSY 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ASAAMTGVAASYARWITTAAAQAEQAAGQAQAAVSAFEAALAATVHPGAVSANRGRLRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 LEQAAAVEEASDTAAANQLMN--NVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 MVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPN----GVVLTNNHVIAGATDINAFSVGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 QTYGVDVVGYDRTQDVAVLQLRGAGGLPSAA--IGGGVAVGEPVVAMGNSG----GQGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 GLPVGQMG-ARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 IATNILGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.9%; Score 448; DB 1; Length 678; 26.5%; Pred. No. 8.1e-16; ative 70; Mismatches 209; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SAAATPGGAVIIAGFPFLDLGNV---------TIGGF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535 PRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSG 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 GNGVGALSVEFGSSAERSSGFGNSGELSTGI------GNSG 449
laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the mycobacterial PPB family.
                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
D -> G (IN REF. 2).
; 209F1593D52533A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 NLGSGNTGDTNFGGGNTGNLNVG--------
                                                                                                                                                                                                                                                                     TIGR; WT1599; -
Tuberculist; Rv1548c; -
InterPro; IRN00030; Microbac PPB.
InterPro; IRR002989; Mycobac pentapep.
Pfam; PF01469; Pentapeptide_2; 11.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                    EMBL; AE007026; AAK45866.1; ALT_INIT.
PIR; A70762; A70762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          678 AA; 66736 MW;
                                                                                                                                                                                                                     EMBL; Z74020; CAA98335.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STALN-H97RV.
COL STA. Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
A COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
A Gordon S. V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
A Badcock K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
A Oliver S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitchead S., Barrell B.G.;
T "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
In Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERGINE S. C. (1551 / Oshkosh; -
STRAIN=CDC 1151 / Oshkosh; -
MEDLINE=22206494; Pubwed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Fatt D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weinfann J.A., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                      Harris
                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                 Shinnick T.M.; "The 65-Kilodalton antigen of Mycobacterium tuberculosis."; J. Bacteriol: 169:1080-1088(1987).
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E -> K (IN REF. 2).

F T (IN REF. 1).

G -> GNNNIG (IN REF. 1).

7247 MW; 97234D5B316C8C7F CRC64;
                                                                                                                                                            Corynebacterineae; Mycobacteriaceae; Mycobacterium
                            01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv0442c/MT0458.
Mycobacterium tuberculosis.
487 AA
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R InterPro; IPR000309; Microbac Dentapep.

R Pfam; PF01469; Pentapeptide 2; 5.

R Pfam; PF01469; Pentapeptide 2; 5.

R Hypothetical protein; Complete protecme.

CONFLICT 40 40 E -> K (IN RE CONFLICT 96 96 1 -> T (IN RE CONFLICT 211 211 G -> GNNNIG (SEQUENCE 487 AA; 47247 MW.
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EMBL; AL021932; CAA17399.1; -.
EMBL; AE006948; AAK44681.1; -.
                                                                                                                                                                                                                                                                   MEDLINE=87137260; PubMed=3029018;
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                  P426<u>1</u>1; 053727;
01-NOV-1995 (Rel. 32,
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Length 487;

DB 1;

Score 445;

14.8%;

Query Match

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                                                                                                                           TNLLGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAG----
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                                                                                       12 FGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSA
                                   Gaps
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann W.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Badcock S.V., Eighmeier K., Bary C.E. III. Tekala F., Davies R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Henraby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Oliver Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                   58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
; Pred. No. 8e-16;
49; Mismatches 181; Indels
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv0878c/MT0901.
Mycobacterium tuberculosis.
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31.9%;
al Similarity 31.99
135; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                       laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
i. SUBCELLULAR LOCATION: Integral membrane protein (Potential).
i. SIMILARITY: Belongs to the mycobacterial PPE family.
"Whole-genome comparison of Mycobacterium tuberculosis clinical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 X 10 AA APPROXIMATE REPEATS
C58BEC607F0675E2 CRC64;
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
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ALA-RICH.
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InterPro, IPR000030; Microbac PPE.
InterPro, IPR002899; Mycobac pentapep.
Pfam, PF01469; Pentapeptide_2; 4.
Pfam, PP00823; PPE, 1.
Hypothetical protein; Transmembrane; Reference Protein; Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Pransmembrane; Reference Prans
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EMBL; AE006977; AAK45143.1; ALT_INIT.
PIR; Z70780; C70780
TIGR; MT0901; --
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443 AA;
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                                                                                                                      MEDINE-99239328; PubMed-8478104; Vega-Lopez F., Brooks L.A., Dockrell H.M., de Smet K.A.L., Thompson J.K., Hussain R., Stoker N.G.; Sequence and immunological characterization of a serine-rich antigen from Mycobacterium leprae."; Infect. Immun. 61:2145-2153(1993).
                                                                                                                                                                                                                                                                                                                                                                                                             Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Shillingworth T., Connor R., Davies R.M., Davies R.M., Duthoy S., Feltwell T., Farser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutherfer S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                  "A Mycobacterium leprae-specific gene encoding an immunologically recognized 45 kDa protein."; Mol. Microbiol. 10:829-838(1993).
                                                                                                                                                                                                                                                     MEDLINE-95020554; PubMed=7934845;
Rinke de Wit T.F., Clark-Curtiss J.E., Abebe F., Kolkon A.H.J.,
Jonson A.A.M., Thole J.E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-SER.
2 X 6 AA REPEATS OF S-V-A-Q-S-E.
                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%; Score 365; DB 1; Length 408; 26.2%; Pred. No. 7.2e-12; tive 74; Mismatches 168; Indels E
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S -> L (IN REF. 2).
H -> D (IN REF. 2).
P -> L (IN REF. 2).
N, 5COC2BEODGEGA9D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
Serine-rich antigen (25L) (45 kDa protein).
SRA OR ML0411 OR MLCL383.14.
Mycobacterium leprae.
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Antigen; Repeat; Complete proteome
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EMBL, X68431; CAA48480.1; -..
EMBL, Z21952; CAA79950.1; -...
EMBL, Z97179; CAB09938.1; -...
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PIR, S33522, S33522.
PIR, S39872, S39872.
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                                                                                  NCBI_TaxID=1769;
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CONFLICT
SEQUENCE
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12;

Gaps

88;

Best Local Similarity 26.28 Matches 117; Conservative

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SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 128
                                                                                                                                                                                                                                                                                                                                    129 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILDPFEEAPEMTSAGG 188
                                                                                                                                                                                                                                                                                                                                                                                               270 LSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAAN-----LGRAASVG 324
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MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                        1 MFDFMVYSPEVNAFLMSRGPGSTPLWGAAEAWISLAEQLMEAAQEVSDTIVVAVPASFAG
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
17-OCT-2003 (Rel. 42, Last annotation update)
14-OCT-2003 (Rel. 42, Last annotation update)
Rypothetical PPE-family protein Rv3018c/MT3098/MT3101
RV3018C OR MT3098/MT3101 OR MTV012.32C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 ALRVPENWATASOPVMATAHSVPAGCSAITTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 LRVPPRPYWPHSPAAGD-IAPPALSQ 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 TQ--PAEEVLTASVAGGSGTGGPAFNE 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis.
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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation strongers Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 LLGQNTPALAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPENTSAGGLLEQA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 FFGINTIPIALNEADYVRMWVQAATVMSAYEAVVGAALVATPHTGPAPVIVKPG----- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 AAVEEASDTAAAN-----QLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPH 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ANEASNAVAAATITPFPWHEIVQFLEETFAAYDQYLSALLSELPA--VAWVWFQLFVD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGSSL------GSSGLGG--GVAA--NLGRAASVGSLSVPQAWAAANQAVTPAARA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 MVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVAAYVPYVAWLVQASADSAAAAGEHEAAAAGYVCALAEMPTLPELAANHLTHAVLVATN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---RSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 ILGFNIIGFIITLASNAQLLTEFAINASYVAVGLLYAIA-GVIDIVVEWVIGNLFGVVPL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPLTSLTSAAERGPGQMLGGLPVGQMGARAGG--GLSGVLRVPPRPYVMPHSPAAGDIAP 403
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                                                                                                                                                                                                                                           -!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 294; 337 and 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 ALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Gaps
[3]
SECUENCE OF 160-374 FROM N.A.
STRAIN-Isolate 50410;
Patki A.H., Dale J.W.;
Patki A.H., Dale J.W.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: Belongs to the mycobacterial PPE family.
-: CAUTION: In strain Oshkosh the gene for this protein is interrupted in position 307 by an IS6110 element.
-: CAUTION: Was originally (Ref.3) thought to be a dihydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.2%; Score 338; DB 1; Length 434; 27.2%; Pred. No. 1.8e-10; ive 54; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; MT3101; ...
Tuberculist; Rv3018c; -.
Tuberculist; Rv3018c; -.
InterPro; IPR00030; Microbac_PPE.
Pfam; PF00823; PPE; ..
Pfam; PF00823; PPE; ..
Hypothetical protein; Complete proteome.
A34 AA; 43029 MW; 41D673C4BD389DD6 CRC64;
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EMBL; AE007129; AAK47427.1; ALT_SEQ.
EMBL; AS07129; AAK47430.1; ALT_SEQ.
EMBL; XS9271; CAA41961.1; ALT_FRAME.
PTR; E70857; F70857.
TICR; MT3098; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 123; Conservative
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S
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STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Debkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=9829597; PubMed=9634230;

Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Kroph A., Mclean J., Moulle S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sultson J.B., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacobary 3. 184:5479-5490(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
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                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%; Score 334; DB 1; Length 463; 25.4%; Pred. No. 3e-10;
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N; 42D9D66A033D0DD8 CRC64;
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv0096/MT0105.
RV0096 OR MT0105 OR MTCV251.15.
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PTR; H70750; H70750.
TICR; MT0108; -.
TUBErCHList; Rv0096; -.
InterPro; IPR000030; Microbac_PPE.
Ffam; PP00823; PPE; 1.
HYDOCHetical protein; Transmembrane; COTRANSMEM 3 23 POTENTIAL.
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                                                                                                                                                                                      Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete genome sequence.'
Nature 393:537-544(1998).
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Best Local Similarity 25.4
Matches 138; Conservative
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MEDLINE-9825987; PubMed=9634230;

MEDLINE-9825987; PubMed=9634230;

MEDLINE-9825987; PubMed=9634230;

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                                                                                338 AVTPAARALPLISLISAAERGPGOMLGGLPVGOMGARAGGGLSGVLRVPPRPYVMPHSPA
                                                 74 MVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 LPIAAA---------V
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                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
MEDLURE-22206494; PubMed=12218036;
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Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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053268; 053269;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv3021c/Rv3022c/MT3106.
RV3021C/RV3022C OR MT3106 OR MTV012.35c/MTV012.36C.
                                                                                                                                                                                                                                                 194 AAVEEASDT----AAANQLMNNVPQALQQLAQPTQ----
                                                                                                                                                                                                                                                                                                                                                                                 | : | : | 230 OLYDFLWYPYYASYGLLLLPFFTP-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L. Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A. Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 435;
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                                                                                                                                  J. Bacteriol. 184:5479-5490(2002).
-!- SIMITARITY: Belongs to the mycobacterial PPE family.
-!- CAUTION: Ref.i sequence differs from that shown due frameshift in position 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prefin; Complete proteome.

99 c 299 (G -> A (IN REF. 2).

117 320 LAGV -> VTGL (IN REF. 2).

226 L -> V (IN REF. 2).

15 AA, 42876 MW, 3B157643EAA8484A CRC64;
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25.3%; Pred. No. 3e-10
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EMBL; AL021287; CAA16107.1; ALT_FRAME.
EMBL; AE007129; AAK47435.1; -
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Tuberculist; Rv3022c; -.
InterPro; IPR000030; Microbac_PPE.
Pfam; Pr00823; PPE; I
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                                                                                                            laboratory strains."
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Matches 123;
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RESULT 12
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RA Ghim S.V., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

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RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

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RA Kobayashi Y., Roetter P., Koningstein G., Krogh S., Kumano M.,

Robayashi Y., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S.,

RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

RA Sekiguchi M., Tamakoshi A., Tanaka T., Tarkamaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Tarkamaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Tarkamaru K.,

RA Voshida K., Voshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

RA Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

RT "The complete genome sequence of the Gram-positive bacterium Bacillus

RT "The Complete genome sequence of the Gram-positive bacterium Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98015415; PubMed=9353931; Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.; Medina N., Vannier F., Roche B., Autret S., Levine A., Seror S.J.; "Sequencing of regions downstream of adda (98 degrees) and citG (289 degrees) in Bacillus subtlis."; Microbiology 143:3305-3308(1997).
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"YAGA and YVAA, HITA-like serine proteases in Bacillus subtilis,
engage in negative autorequiation and reciprocal cross-regulation of
ykdA and yvtA gene expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20158875; PubMed=10692364;
Noome D., Howell A., Devine K.M.;
"Expression of ykdA, encoding a Bacillus subtilis homologue of HtrA, is heat shock inducible and negatively autoregulated.";
J. Bacteriol. 182:1592-1599(2000).
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    Bacteriol. 183:654-663(2001).
    FUNCTION: May be involved in processing, maturation,
of extracellular enzymes.

                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                PATA BACSU STANDARD; PRT; 458 AA. 09R9II; 035021; 035039; PRT; 458 AA. 09R9II; 035031; 035039; PREB-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 41, Last annotation update) 10-0CT-2003 (Rel. 41, Last annotation update) 10-0CT-2003 (Rel. 41, Last annotation update) 10-0CT-2003 (Rel. 41, Last annotation update) 10-0CT-2003 (Rel. 41, Last annotation update) 10-0CT-2003 (Rel. 41, Last annotation update) 10-0CT-2003 (Rel. 41, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 42, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, Last annotation update) 10-0CT-2003 (Rel. 43, L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 TSQNNTFGTGGGSSSESESGTGSGVIFKKDSDKAYIITNNHVVEGANKLTV-TLYNGETE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 LGYNNAV------GAGTGIVI---DPNGVVLTNNHVIAGATDINAFSVGSGQTY 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91
SUBCELLULAR LOCATION: Membrane-bound (Potential).

Inductron: Induced by heat shock during exponential growth and by heterologous amylases at the transition phase of the growth cycle. Negatively regulates its own expression.

NESCELLAMBOUS: Inactivation results in compensating overexpression of http. especially during stress conditions.

SIMILARITY: Conclains 1 PDZ/DHR domain.

CAUTION: Ref.2 and Ref.3 sequences differ from that shown due to frameshifts in positions 87 and 246 that produce two separate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 LSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGL-PVGQMGARAGGGLS-GVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384 RVPPRPYVWPHSPAAGDIAPPALSQDRFADFPALPLDPSA----MVAQVGPQVVNI-NTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 TAKLVGSDTITDLAVLEISGKNVKKVASFGDSSQLRTGEKVIAIGNPLGQQFSGTVTQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDAPVSYEAGRÓ---ETASÁLEMEKQETÁVKKEKKRRAAWLSPI--LGGIIGGGLMLGI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
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77551045A865ASCD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
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Pred. No. 1.2
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InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001203; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1C.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00834; PROTEASESCC.
SWART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF188296; AAF03153.1; -.
EMBL; 293941; CAB07968.1; ALT_FRAME.
EMBL; 293941; CAB07969.1; ALT_FRAME.
EMBL; 299120; CAB15290.1; ALT_FRAME.
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92
458
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356
187
217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98295987; PubMed-9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gorlon S.V., Eiglaneler K., Gas S., Barry C.E. III, Tekaia F., Bacham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Horisby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulton J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPPEINSARMYAGPGSASLVAAAQ----MWDS---VASDLFSAASAFQSVVWGLTVGSWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 178;
                                                                                                                                                                                                     Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Bacteriol. 184:5479-5490(2002).
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InterPro, IPR000030; Microbac_PPE.
Pfam, PF00823; PEF, II.
Hypotherical protein; Complete proteome.
SEQUENCE 178 AA; 19811 MW; 8BE1FC025ABFBEA6 CRC64;
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Best Local Similarity 35.9%; Pred. No. 1.3e-05;
Matches 65; Conservative 25; Mismatches 76;
                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPB-family protein Rv3429/MT3533.
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MEDLINE=22206494; PubMed=12218036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 79; Gaps
                                                                                                                                                                                                                       Embryophyta; Tracheophyta;
edons; core eudicots; rosids;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i. FUNCTION: Probable serine protease.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Kaneko I., Katoh I., Asamizu E., Sato S., Nakamura Y., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Protease Do-like 8, chloroplast precursor (EC 3.4.21.-).
DEGRB OR ATSG39830 OR K13H13.1.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARGE RELAY SYSTEM (POTEN
CHARGE RELAY SYSTEM (POTEN
CHARGE RELAY SYSTEM (POTEN
A986FC1387670AFF CRC64;
                                                                                                                                                                                                                        Bukaryota, Viridiplantae, Streptophyta, Embryophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core e
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.5%; Score 225.5; DB 1;
88.1%; Pred. No. 8.5e-05;
ve 41; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to peptidase family S2C.
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PROTEASE DO-LIKE
SERINE PROTEASE.
                                                                                                     448 AA
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Kieselbach T., Bystedt M., Schroeder W.P.;
Submitted (OCT-2000) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PDZ.
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InterPro; IPR001940; Peptidase_S1C.
Pfam; PF0059; PDZ; 1.
PRINTS; PR0089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
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Hydrolase; Serine protease; Trans
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nes 87; Conservative
                                                                                                     STANDARD;
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214
292
448 AA;
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188 G 188
                         177 Ġ 177
                                                                                                    DEGS ARATH
Q9LUIO;
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Tabata S.;
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DEG8_ARATH
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SEQUENCE FROM N.A.
STRAIN=0.15:147 / RIND 0509952;
STRAIN=0.15:147 / RIND 0509952;
Bayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo B., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Secherichia coli "Complete genome sequence of enterchemorrhagic Escherichia coli O15:147 and genomic comparison with a laboratory strain K-12.";
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Vogel R.F., Entian K.-D., Mecke D.;
"Cloning and sequence of the mdh structural gene of Escherichia colicoding for malate dehydrogenase.";
Arch. Microbiol. 149:36-42(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bazan J.F., Fletterick R.J., "Structural and catalytic models of trypsin-like viral "Structural and catalytic models of trypsin-like viral Semin. Virol. 1:311-322(1990).
-!- SUBCELLUIAR LOCATION: Periplasmic (Potential).
-!- SIMILARITY: Belongs to peptidase family S2C.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
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V -> E (IN REF. 6).
D091B4D65E8FEICC CRC64;
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Ecodene; EG11652; hhoB.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001478; PD2.
InterPro; IPR001478; PD2.
InterPro; IPR01954; Peptidase_S1.
InterPro; IPR01954; Pptidase_S1C.
Pfam; PF00599; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMRT; SM00228; PD2; 1.
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EMBL; AE005551; AAG58363.1; -.
EMBL; AP002564; BAB37531.1; -.
EMBL; M24777; -; NOT ANNOTATED_CP
PIR; U5142; D31142.
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Hydrolase; Serine protease;
SIGNAL
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281 3
96
126
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253
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355 AA;
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CONFLICT
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SEQUENCE FROM N.A.

RX MEDILINE=210749315, PubMed=11206551;

RA PEDILINE=210749315, PubMed=11206551;

RA Perra N.T., Plunkett G. III. Burland V., Mau B., Glaener J.D., RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., A Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., A Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Lin J., Yen G., Schwartz D.C., T. "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; N 151
                                                                                                                                                                                                                                                                                                                                                                                                                                      525 MGNSGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNG
                                                                             378 GLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPS-AMVAQVGPQ----V
                                                                                                                                                                                                                                                                                                                                                                                         474 -- AFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAI -----GGGVAVGEPVVA
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Rlaty M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Protecbacteria, Gammaprotecbacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 83334;
    41 VSSVKVTQDWKSNLHELAVKSVPSTTRRILLTSLFMNLCFNPSRYLSALALGD--
                                                                                                                                                                                                                                   433 VMI-----NTKLGYNNAV----GAGTGIVIDPNGVVLTNNHVIAGATDIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Drotease degS precursor (EC 3.4.21.-).
DEGS OR HOB OR HTMH OR B3235 OR Z4594 OR ECS4108.
Escherichia coli, and
Escherichia coli 0157:H7.
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STRAIN-K12 / W3110;
MEDLINE-96165272; PubMed-8576051;
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STRAIN=K12 / MG1655;
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P31137;
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EMBL; AE001678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMIL outstation. The Detwoen Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                   77 RTLGSGVIMDQRGYIITNKHVINDADQI-IVALQDGRVFEALLVGSDSLTDLAVLKINAT 135
                                                                               561
   ---GTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P., Schneider S., Pohl T., Essig A., Marre R., Melchers K.; "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linner K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Melson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Bisen J., Fraser C.M.;
                                                          GGLPSAAIGGGVA--VGEPVVAMGNSGGQGGTPRAVPGRVVALGQTV-QASDSLTGAEET
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=9920666; PubMed=10192188; MEDLINE=99206666; PubMed=10192188; Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314 (2000).
                                                                                                                                                                                                                                                                                                                           Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
                                                                                                                                                                                                                                       Q9ZGTO; Q9JQD7; Q9KIW4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HTRA OR CPN0979 OR CP0877 OR CPB1016.
                                                                                                                                     562 LN-----GLIQFDAAIQPGDSGGPVVNGLGQVVGMNT 593
                                                                                                                                                                                                                            488 AA.
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MEDLINE=20330349; PubMed=10871362;
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DEGP CHLPN
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POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
PDZ 1.
CHACE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
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8.6%; Pred. No. 9.9e-05;
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InterPro; IPR001254; Peptidase S1.
InterPro; IPR001940; Peptidase S1C.
Pfam; PF00089; PT2/2.
PRINTS; PR00894; PROTEASESC.
SWART; SW00228; PDZ; 2.
SWART; SW00220; TT2/P SPC; 1.
PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Sepeat; S
                   AE002246; AAF38665.1; -. AP002548; BAA99186.1; -. AE017160; AAP98945.1; ALT_INIT.
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Best Local Similarity
Matches 83; Conservative
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PIR; H86612; H86612.
MEROPS; S01.273; --
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238
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June 30, 2004, 16:43:31; Search time 15.5767 Seconds (without alignments) 3680.509 Million cell updates/sec
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Perfect score: 3007
Sequence: 1 HMHHHHHHMVDFGALPPEIN......SGGPVVNGLGQVVGMNTAAS 596
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	B7060	H7074	C705	F7098	G7092	84717	A8724	A7093	H7093	B7093	H8705	G1092	B7062	F7056	B7093	C7093	A7064	G7088	H7050	H7092		A7088	C7058	D7092	A7050	E7067	A7066	D7057	E7096
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RESULT 1 Bytobable PPE protein - Mycobacterium tuberculosis (strain H37RV) Cybecies: Mycobacterium tuberculosis C;Becies: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: B70608 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Raidandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome s A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Residues: preliminary; nucleic acid sequence not shown; translation not shown A;Rosidues: L-391 <col/> A;Cross-references: GB:Z93777; GB:AL123456; NID:g3261726; PIDN:CAB07839.1; PID:e311073; I A;Bxperimental source: strain H37RV C;Genetics: PPE	Query Match 64.8%; Score 1949; DB 2; Length 391; Best Local Similarity 100.0%; Pred. No. 1.3e-95; Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 9 mVDFGALPBEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG 68	Qy 69 ŚSAGLMVAAASPYVAWMSYTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 128 	Qy 129 LIATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPENTSAGG 188 	Qy 189 LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248	Qy 249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSG 308 	Qy 309 IGGGVAANIGRAASVGSISVPQAWAAANQAVTPAARAIPLISITSAAERGPGQMLGGLPV 368 	Qy 369 GQMGARAGGGLSGVLRVPPRPYVWPHSPAAG 399	
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Best Local Similarity
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Nature 393, S37-54, 1998
A; Starses, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
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probable PPE protein - Mycobacterium tuberculosis

probable PPE protein - Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

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C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

Rajandream, M.A.; Rogers, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Rajandream, M.; Rogers, J.; Rutter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Piterence number: A70500; MUID:98295987; PMID:9634230

A;Accession: C70568
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                                                                                                       probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H70741
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55.1%; Score 1656.5; DB 2; Length 396;
Best Local Similarity 85.1%; Pred. No. 3.1e-80;
Matches 338; Conservative 18; Mismatches 34; Indels 7;
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GOMGARAGGGLSGVLRVPPRPYVMPHSPAAG 391
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A;Cross-references: GB:Z95390; GB:AL123456; NID:g3261766; PIDN:CAB08702.1; PID:e316074; A;Experimental source: strain H37Rv C;Genetics:
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A/Experimental source: strain H37Rv
C/Genetics:
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F701e, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go F, F.Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holrn Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 339, 537-544, 1998
A, Authors. Sqares, F.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987; PMID:9634230
A, Scassion: F70983
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                             52.6%; Score 1583; DB 2;
llarity 81.5%; Pred. No. 2.3e-76;
Conservative 20; Mismatches 47;
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submitted to the EMBL Data Library, June 1993
A; Description: Isolation and characterisation of a 34KDa protein of Mycobacterium paratul A; Reference number: 847170
A; Reference number: 847170
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-361 < CCAM>A; Residues: 1-361 < CCAM>A; Cross-references: EMBL: Z23092; NID: 9505550; PIDN: CAA80638.1; PID: 9505551
C; Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryps
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Holroyd,
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: My Mycobacterium leprae
C;Accession: A87242
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; F.; Davries, R.M.; Devilin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyy atture 409, 1007-1011, 2001
A;Atture, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; A;Ritle: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1.354 <STO>
A;Cross-references: GB:AL450380; NID:g13093863; PIDN:CAC32191.1; GSPDB:GN00147
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                                                                                                                                                                                                                                                                                                                                                 Similarity 66.0%; Score 778.5; DB 2; Length 361; Similarity 66.0%; Pred. No. 4.1e-34; S. Conservative 28; Mismatches 37; Indels 15
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                                                                             576
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       GVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGV 147
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                                                                                                                          1 MDFGALPPEVNSVRMYAGPGSAPMVAAASAWNGLAAELSSAATGYETVITQLSSEGWLGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 GTQAAAVATAAGTAQSTLTEMITGLPNALQSLTSPLLQSS-NGPLSWLWQILFGTPNFPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 -----TVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 QNGVRAMSSLGSSLGSSGLGGGGVAANLGRAASVGSLSVPQAWAA-ANQAVTPAARALPLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFOSVVWGLTVGSWIGS
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347170
hypothetical protein 34K - Mycobacterium paratuberculosis
hypothetical protein 34K - Mycobacterium paratuberculosis
C;Species: Mycobacterium paratuberculosis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Dec
C;Accession: S47170
R;Cameron, R.M.; Stevenson, K.; Inglis, N.F.; Klausen, J.; Sharp, J.M.
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TVSAAPEAAPGSLLGGLPL---AGAGGAGAGP-RYGFRPTWMARPPFAG 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.9%; Score 779.5; DB 2; Length 393; Best Local Similarity 43.7%; Pred. No. 4e-34; Matches 179; Conservative 65; Mismatches 129; Indels 37
                                                                                                                                                                                                                      596
                                                                                                                                                                                                                                                                   208 SGGPVVNGLGQVVGMNTAAS 227
                                                                                                                                                                                                                   577 SGGPVVNGLGQVVGMNTAAS
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PIDN:CAA17728.1; PID:e1254618
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A,Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable PPE protein - Mycobacterium tuberculosis (strain H37kV)
C;Species: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 IGSALGGTPWVAPPPAVAAG----MPGMPFGTWGGQGFG-----RAVPQYGFRPNFVAR 398
                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-403 <COL>
A;Residues: 1-403 <COL>
A;Cross-references: GB;AL022021; GB;AL123456; NID:g3250699; PIDN:CAA17728.1; E;Enperimental source: strain H37Rv C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 BASASMTAAAAPYVAMMSVTAVRAEQAGAQAEAAAAYEAAYEAAFAATVPPPVIEANRAQIMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 IATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 IATINVILGONAPAIAATEAQYAEMASQDANAMYGYAGASAAAT-QITPFTEPVQTINASGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 KLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSM-TNTLS---SMLKGFAPAAAAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 QTAAQNGVRAMSSLGSSL----GSSGLGGGVAANLGRAASVGSLSVPQAWAANQAVTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 403;
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24.5%; Score 737; DB 2; Length 423;
Best Local Similarity 41.8%; Pred. No. 7.6e-32;
Matches 183; Conservative 50; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 24.5%; Score 737.5; DB 2; Best Local Similarity 42.6%; Pred. No. 6.7e-32; Matches 181; Conservative 60; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPAAG 399
A; Accession: H70931
A; Status: prelimina
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                                                                                                                                                                                                                                                                                                                                                  R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H70931
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Peltwell, T.; Gentles, S.; Hamin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atthors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
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                                                                                                                                                              probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VATNIFGONTPAJAATEAHYAEMWAQDAAMYGYAGSSATA-SQLAPFSEPPQTINPSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 RSPISNMVSMANNHMSMTNSGVS-----MTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 AAQSAVVAQAAGAASSDITAQLSQLISLLPSTLQSLA--TTATATSASAG--WDTV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 SSL-GSSLGS-SGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 AERGPGOMLGGLPVGOMGARAGGGL----SGVLRVPPRPYVMPHSPAAGDIAPPALSQD
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S. S.

genome

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Qy 223 TQGTTPSSKLGGLWKTVSPHRSPISNNVSWANNHMSWINSGVSMINTLSSMLKGFAPA 280 240 QTAVPDSSSAAAPQLMGGFAQHLSPINDTLSMINNHAGMANAGLSLVNGMGSAMKSLAP- 298	281	341 PAARALPLTSLTSAABRGPGQML-GGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSP	359 AATRALSPARVAVATESESAPLLGGGLPMARMVPGGGSGTGGVNTALKLGPRAFVMPRNP 397 AAG 399	Db 419 AAG 421 RESULT 12	G70925 G70925 Probable PPE protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999	C;Accession: G70925, R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, ; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.	Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Telle: Deciphering the biology of Mycobacterium tuberculosis from the complete genor A;Reference number: A70500; MUID:98295987; PMID:9634230	A, Accession: Dyellminary, nucleic acid sequence not shown, translation not shown A, Molecule type: DNA A, Residues: 1-408 < COD- A, Residues: 1-408 < COD- A, Cross-references: GB: Z74024; GB: Ml123456; NID: G3250700; PIDN: CAA98377.1; PID: e130102 A, Experimental source: strain H37Rv C, Genetics: A, Genetics: A, Genetics:	P.R.; Holroy	s, R.; Sq Qy 10 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS 69	Qy 70 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 129	Qy 130 IATNLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLDFEEAPEMTSAGGL 189	Qy 190 LEQAAAVEEASDTAAANQLMNNVPQALQQ-LAQPTQGTTPSSKL 232	Db 180 AGQAAATVSSTVPPLATTAAVPQLLQQLSSTSLIPWYSALQQMLAENLLGLTPDNRMTIV 239 Qy 233GGLWKTVSPHRSPISNWVSMANNHNSMTNSGVSMTNTLSSMLKGFAPAAA 283	240 RLLGISYF	Qy 284 QAVQTAAQNGVRAMSSLGSSLGSSGLGGGVAANLGRAASVGSLS 327	328 VPQAWAA	RGTAENALLRGFP
: :: : : : :	70 SAGLANVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPFVIAENRAELMIL 129 	130 IATNILIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLIPFEEAPEMTSAGGL 189 : : :	190 LEGABAVEEASDTABANQLMUNVPQALQQLAQPTQTTPS 229 	230 SKLGGLWKTVSPHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTA 289 	SLGSSGLGGG-VAANLGRAASVGSLS	328 VPQAWAAANQAVTPAARALPLISLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVLR 384	385 VPPRPYVMPHSPAAGDIA 402 	protein [imported] - Mycobacterium leprae Mycobacterium leprae Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001	<pre>Parkhill, J.; James, K.D.; Thomson, N.R. Duthoy, S.; Feltwell, T.; Fraser, A.; J</pre>	butter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, ssive gene decay in the leprosy bacillus. number: A86909; MUID:21128732; PMID:11234002 H87056	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-421 <sto> A;Cross-references: GB:AL450380; NID:gl3093150; PIDN:CAC31563.1; GSPDB:GN00147</sto>	3%; Score 731	.6e-31; les 160;	9 MVDFGALPPEINSARMYAGPGSASIVAAAQMWDSVASDIFSAASAFQSVVWGLTVGSWIG 68	SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 1	60 ESAAALAERVIPYEKWIIQNAASAELTAIQLIVAANAYETAFIMIVPPIMVEVNRAQACL 119 129 I.TATNII.GONTPATAVNRARYGRAWAQDAAAMFGYAAATATATTI.PFREAPRMISAGG 188	:	189 LVPQALQQLAQP 222

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A)Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17730.1; PID:e1254620
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: PPE
           A;Residues: 1-413 <COL>
A;Cross-references: GB:Z95436; GB:AL123456; NID:g3261770; PIDN:CAB08826.1; PID:e316565;
A;Cross-references: GB:Z95436; GB:AL123456; NID:g3261770; PIDN:CAB08826.1; PID:e316565;
C;Genetics:
A;Gene: PPE
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Ual-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70932
B;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A7050; MUID:98295987; PMID:9634230
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                                                                                                                                                                                        Length 413;
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAA---AAQAVQT---
                                                                                                                                                                                     Ouery Match
23.3%; Score 702; DB 2; L
Best Local Similarity 39.1%; Pred. No. 5.1e-30;
Matches 168; Conservative 61; Mismatches 145;
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Best Local Similarity 38.4
Matches 174; Conservative
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70625
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A.Cross-references: GB:Z92539; GB:AL123456; NID:g3261714; PIDN:CAB06873.1; PID:e304546;
A.Experimental source: strain H37Rv
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Centles, S.; Hamlin, N.; Holroyd, Sajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295997; PMID:9634230
A;Accession: F70560
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                                                                                                                                  probable PPB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 VDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDFGALPPEINSARMYAGAGAGPMMAAGAAWNGLAAELGTTAASYESVITRLTTESWMGP
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YGFRLAVMQRPPFAG
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70 SAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMIL 129
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1 HMHHHHHHWUDFGALPPEIN......SGGPVVNGLGQVVGMNTAAS 596
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB_pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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	ΠD	US-09-287-849-26	US-09-886-349A-20	US-10-359-460-26	US-10-098-732A-20	US-10-369-983-21	US-10-369-983-15	US-10-369-983-14	US-10-369-983-13	US-10-098-732A-65	US-10-369-983-12	US-10-369-983-18	US-10-369-983-17	US-10-369-983-16	US-09-886-349A-18	US-10-098-732A-18
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ALIGNMENTS

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Sequence 26, Application US/9287849

Sequence 26, Application US/9287849

Patent No. US2002000945941

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens

TITLE OF INVENTION: And Their Uses

FILE REFERENCE: 014058-009200S

CURRENT APPLICATION NUMBER: US 08/9287, 849

CURRENT FILING DATE: 1999-04-07

PRIOR APPLICATION NUMBER: US 08/942,578

PRIOR APPLICATION NUMBER: US 09/025,197

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

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ORGANISM: Artificial Sequence
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Best Local Similarity
RESULT 1
US-09-287-849-26
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Indels

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Mismatches

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1 HMFHFHFHFWVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWG
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                                                    HMHHHHHHHHHWDFGALPPEINSARMYAGPGSASIVAAAQMWDSVASDLFSAASAFQSVVWG
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Publication No. US20040086523A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Corrixa Corporation
ITILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
CURRENT APPLICATION NUMBER: US 09/597,796
FILE REPLIAND DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/597,796
PRIOR APPLICATION NUMBER: US 60/265,737
PRIOR FILING DATE: 2001-06-10
NUMBER: OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 596
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 Mismatches
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ORGANISM: Artificial Sequence
 Matches 596; Conservative
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Canta Corporation
APPLICANT: Canta Corporation
APPLICANT: Canta Corporation
APPLICANTON: Tation of Mycobacterium tuberculosis Antigens
FILE REFERENCE: 014059-009020US
CURRENT FILING DATE: 10459-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/026,556
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/026,566
PRIOR APPLICATION NUMBER: US 09/026,566
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                                                           61 LTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIA
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Publication No. US20030147911A1
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Artificial Sequence
               ORGANISM: Artificial Sequence
                                                                                                                                Best Local Similarity 100.
Matches 596; Conservative
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US-10-098-732A-20

Sequence 20, Application US/10098732A

Publication No. US20030172294A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Steiky, Yasir
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leichmania Antigen
FILE REFERENT SPLICATION NUMBER: US/10/098,732A

CURRENT APLICATION NUMBER: US 60/275,837

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 80

SEQ ID NOS: 80

LENGTH: 596
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                                                           FEATURE:

, OTHER INFORMATION: Description of Artificial Sequence:bi-fusion US-10-359-460-26
                                                                                                                                100.0%; Score 3007; DB 14; Length 596; 100.0%; Pred. No. 5e-202; ive 0; Mismatches 0; Indels 0;
SEQ ID NO 26
LENGTH: 596
TYPE: FT
ORGANISM: Artificial Sequence
                                                                                                                              Query Match
Best Local Similarity 100.
Matches 596; Conservative
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; Sequence 21, Application US/10369983
; Publication No. US20030235593A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Guderian, Jeff
; APPLICANT: Goderian, Jeff
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REPERENCE: 014058-009081US
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2002-02-18
; PRIOR PILING DATE: 2002-02-15
; NUMBER: OF SEQ ID NOS: 22
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 21
LENGTH: 729
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; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion; OTHER INFORMATION: protein TDH9-Ra35 (designated MTB59F) US-10-098-732A-20
                                                                                                            100.0%; Score 3007; DB 14; Length 596; 100.0%; Pred. No. 5e-202; ive 0; Mismatches 0; Indels 0;
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Squence 15, Application US/10369983
Publication No. US2003023559341
GBNERAL INPORMATION:
APPLICANT: Skelky, Yasir
APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT APPLICATION NUMBER: US/020-02-18
FRIOR APPLICATION NUMBER: US/020-02-18
FRIOR FILING DATE: 2002-02-18
SOFTWARE: PatentIn Ver. 2.1
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OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: MTB81F (MTB72F-DPV)
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                                                                  Length 729;
          ; OTHER INFORMATION: Description of Artificial Sequence: MTB72F
US-10-369-983-21
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                                                            Query Match 98.0%; Score 2946; DB 15; Best Local Similarity 100.0%; Pred. No. 1.2e-197; Matches 588; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence:fusion protein
CTHER INFORMATION: WTB83F (WTB72F-MTI)
US-10-369-983-14
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APPLICANT: Guderian, Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Red Green of APPLICANT: Red Jeff
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
FILTE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILTE OF INVENTION: 104056-00908108
CURRENT APPLICATION NUMBER: US/10/369,983
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR PLING DATE: 2002-02-15
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98.0%; Score 2946; DB 15;
100.0%; Pred. No. 1.4e-197;
iive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 825
  Query Match
Best Local Similarity 100.
Matches 588; Conservative
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US-10-088-732A-65

Sequence 65, Application US/10098732A

PUBLICATION NO US20030175294A1

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Corixa Corporation
TILE OF INVENTION: Leishmania Antigen
FILE REPRENCE: 014058-012010US
FILE REPRENCE: 014058-012010US
FILE REPRENCE: 02010US
CURRENT APLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 65
LENGTH: 930
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:WTB72F-WAPS
OTHER INFORMATION: (1951) fusion construct, TB WIB72F (Ra12-TbH9-Ra35)
OTHER INFORMATION: (1954) fusion construct, TB WIB72F (Ra12-TbH9-Ra35)
OTHER INFORMATION: (15A or MAPS)
US-10-098-732A-65
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US-10-369-983-13

i Sequence 13, Application US/10369983

j Publication No. US20030235593A1

j GENERAL INFORMATION:
    APPLICANT: Skeiky, Yasir
    APPLICANT: Reed, Steven
    APPLICANT: Reed, Steven
    APPLICANT: Responsation
    TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
    FILE REPERBNCE: 014058-009831US
    CURRENT FILING DATE: 2003-02-18
    PRIOR FILING DATE: 2003-02-18
    PRIOR FILING DATE: 2002-02-15
    NUMBER OF SEQ ID NOS: 22
    NUMBER OF SEQ ID NOS: 22
    NUMBER OF SEQ ID NOS: 22
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US-10-369-983-13
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   Length
                                   Indels
98.0%; Score 2946; DB 15;
100.0%; Pred. No. 1.4e-197;
iive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
FEATURE:
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SEQ ID NO 13
LENGTH: 875
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Publication No. US2003023553A1

GENERAL INFORMATION:
APPLICANT: Skeiky. Yasir
APPLICANT: Skeiky. Jeff
APPLICANT: Guderian, Jeff
APPLICANT: Gred, Steven
TITLE OF INVENTION: Pusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-00908108

CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT FILING DATE: 2003-02-18

PRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22
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US-10-369-983-12
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Similarity 100.0%; Pred. No. 1.6e-197; 88; Conservative 0; Mismatches 0;
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Sequence 18, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skelky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US 60/357,351
FRIOR APPLICATION NUMBER: US 60/357,351
FRIOR FILING DATE: 2002-02-18
FRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.1
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98.0%; Score 2946; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-197;
Matches 588; Conservative 0; Mismatches 0;
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APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeff

APPLICANT: Guderian, Jeff

APPLICANT: Guderian, Jeff

APPLICANT: Gorixa Corporation

TILE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis

TILE REPRENCE: 014058-0090410S

CURRENT APPLICATION NUMBER: US/10/369,983

CURRENT APPLICATION NUMBER: US 60/357,351

PRIOR FILING DATE: 2002-02-15

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 16

LEMOTH: 1154

TYPE: PRT

CORCANISN: Artificial Sequence

FEATURE:

CONCANISN: Artificial Sequence
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US-10-369-983-16
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11 Similarity 100.0%; Pred. No. 2.2e-197;
588; Conservative 0; Mismatches 0;
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US-10-369-983-16
US-10-369-983-16
Sequence 16, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION
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US-10-369-983-17
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ORGANISM: Artificial Sequence
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Query Match
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Matches ∷587; Conservative
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SEQ ID NO 18
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                                                                   MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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202 SSAGLMVAAASPYVAMMSVTAGQAELTAAQVRVAAAAXETAYGLTVPPPVIAENRAELMI
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APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITILE OF INVESTION: Fusion Proteins of Mycobacterium Tuberculosis
TITILE OF INVESTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REPERENCE: 014058-09070US
CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRICR APPLICATION NUMBER: US 09/597,796
PRICR APPLICATION NUMBER: US 09/597,796
PRICR PRILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 729
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US-09-886-349A-18
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99.8%; Pred. No. 2e-197;
tive 1; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 99.8†
Matches 587; Conservative
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US-10-098-732A-18
US-10-098-732A-18
is Sequence 18, Application US/10098732A
is Publication No. US20030175294A1
is Publication No. US20030175294A1
is GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Goderian, Jeffrey
APPLICANT: Gorixa Corporation
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.1
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US-10-098-732A-18
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ORGANISM: Artificial Sequence
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SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261	LIAINLLGQNTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG 188	LIATNILGONTPALAVNEAEYGEMWAQDAAAMFGYAAATATATTLLFFREAPEMTSAGG 321	LLEQAAAVEEASDIAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248	LLEQRAAVBEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381	MVSMANNHMSMINSGVSMINTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 308	MVSMANNHMSWINSGVSWINTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 441	LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV 368		GQMGARAGGGLSGVLRVPPRPYWPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV 428	GQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV 561	GPQVVIINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGOTYGVDVV 488	GPQVVNINTKLGYNNAVGAGTGIVIDENGVVLTNNHVIAGATDINAFSVGSGQTYGVDVV 621	GYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTFRAVPGRVVALGQT 548	GYDRTQDVAVLQLRGAGGLFSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQT 681	VQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGNNTAAS 596	VQASDSLTGABETINGLIQFDAAIQPGDAGGPVVNGLGQVVGNNTAAS 729	
202 SS	129 LI.	262 LI	189 LL	322 LL	249 MV	382 MV	309 LG	442 LG	369 GO	502 GQI	429 GP(562 GP(489 GYI	622 GYI	549 VQ	682 VQ2	
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- protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence:
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Issued Patents AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	quence 26,	7	7	22,	10	quence 102	10	quence 102	10,	11	20,0	Sequence 111, App	equence 106	equence 111	equence 109	104	equence 109	Sequence 104, App	equence 109	ω̈	equence 91,	92	91,	92	91,	79	æ
ΩI	-09-287-849-	-09-223-040-	-09-287-849-	-09-287-849-2	-08-818-112-10	-818-111-1	-09-056-556-10	-072-596-10	-09-072-967-10	8-112-11	-08-818-111-10	-09-056-55	2-596-10	-09-072-967-11	-08-818-112-10	8-111-10	-09-056-556-10	2-596-10	-09-072-967-1	-09-287-849-	-08-818-112-9	-08-818-111-9	-556-9	-09-072-596-9		-7	8-
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79,	Sequence 79, App. Sequence 126, App	Sequence 126, App Sequence 16, Appl		142,		Seguence 15, Appl	15,	~	Sequence 208, App	Sequence 92, Appl	Sequence 114, App	109,	Sequence 114, App
US-09-056-556-79 US-09-072-596-80	US-09-072-967-79 US-09-073-009-126	US-09-073-010-126 US-09-287-849-16	US-09-287-849-12 US-09-073-009-142	US-09-073-010-142	US-09-477-135A-131	US-09-073-009-15	US-09-073-010-15	US-08-311-731A-57	US-08-311-731A-208	US-09-050-739-92	US-08-818-112-114	US-08-818-111-109	US-09-056-556-114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LIVGSWIGSSAGLMVAAASPYVAMMSVIAGQAELIAAQVRVAAAAYETAYGLTVPPPVIA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
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OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
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Best Local Similarity 100.0%; Pred. No. 1.3e-219;
Matches 596; Conservative 0; Mismatches 0; Indels 0
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RESULT 1
US-09-287-849-26
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HERERAL INFORMATION:

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Baced, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Carixa Corporation
TITLE OF INVENTION: and Their Uses
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TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: 1999-04-07
TITLE OF INVENTION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-10-01
PRIOR PLILING DATE: 1997-10-01
PRIOR PLILING DATE: 1999-04-07
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PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-12-30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 729
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                                                                                                                        LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQWLGGLPV 368
LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381
                                                                                                                                                                                                                                                                                                                           GPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVV 621
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                                                                               MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAARQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                               GOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV
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Patent No. 6627198
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APPLICANT: Skeiky, Yasir
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REPERENCE: 014058-00901008
CURRENT APPLICATION NUMBER: US/09/223,040
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
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      ENRAELMILIATNILGONTPAIAVNEAEYGEMWAQDAAMFGYAAATATATLLPFEEA 180
                                                                                                                                                   PHRSPISNIWVSMANNIHMSMINSGVSMINTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSL
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                                                                                     PEMTSAGGLLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVS
                                                                                                                            PHRSPISNMVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSL
                                                                                                                                                                                                             GSSLGSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPG
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                                                                                                                                                                                                                                                                                                                                                                        PSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSG
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Best Local Similarity 99.8%; Pred. No. 1.7e-214;
Matches 587; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/09223040; Patent No. 6544522; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-223-040-2
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LENGTH: 729
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19; Mismatches
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METITLE OF INVENTION: COMPOUNDS OF
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 107, Application US/08818112
Patent No. 6290969
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatil
OPERATING SYSTEM: PC DOG,
    Conservative
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CITY: Seattle
STATE: Washington
COUNTRY: USA
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APPLICANT: Reid, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Alderson, Mark

APPLICANT: Alderson, Mark

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

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APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

APPLICANT: Campos-Neto, Antonio

BRIOR PRING APPLICATION NUMBER: US 08/922,78

PRIOR PRING DATE: 1998-02-18

PRIOR PRING DATE: 1998-04-07

PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR APPLICATION NUMBER: US 09/223,040

PRIOR PRING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 46

SSEQ ID NO 22

LENGTH: 600
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                                                                                                              LLEGAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
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SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 261
                                                                                                                                                LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381
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                                      LIAINLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                        262 LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLPFEEAPEMTSAGG
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                                                                                                                                                                                        MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 600;
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Pred. No. 6.7e-146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/09287849
Patent No. 6627198
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Best Local Similarity
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                                                                      1 HMHHHHHHWVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWG
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Gaps
67;
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81; Indels
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6300 Columbia Center, 701 Fifth Avenue
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ZIP: 98104-7092
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               LENGTH: 391 amino acids TYPE: amino acid STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 391; Conservative
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US-08-818-111-102
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STREET: 63
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64.8%; Score 1949; DB 3; L
Best Local Similarity 100.0%; Pred. No. 9.4e-140;
Matches 391; Conservative 0; Mismatches 0;
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILLING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: TWARTZIK, Daniel R.
ANDMBER OF SEQUENCES: 148
                                                       ATTORNEY/AGENT INFORMATION:

NAME: MAKI, DAVIG J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.411C6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEPAX: (206) 622-4900

INFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:

LENGTH: 391 amino acide
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Patent No. 6338852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                      LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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Washington
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US-08-818-112-107
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US-08-818-111-102
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/818,111

FILING DATE: 13-MAR.1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: MAKI, DATIG J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET WUMBER: 210121.417C6

TELECOMONICATION INFORMATION:

TELECOMONICATION INFORMATION:

TELECOMONICATION INFORMATION:

TELECOMONICATION INFORMATION:

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TELECOMONICATION INFORMATION:

TELECOMONICATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:
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TREATME

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COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 391 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                 STREET: 6300 Colum
CITY: Seattle
STATE: Washington
INVENTION:
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Matches 391; Conserva
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US-09-072-967-107
  LITLE OF
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                                                                                                           CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,556

FILING DATE: 07-APR-1998

CLASSIFICATION:

ATTORNEY/AGANT INPORMATION:

NAME: MAXA, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 31,1392

REFERENCE/DOCKET NUMBER: 31,1392

REFERENCE/DOCKET NUMBER: 31,1392

TELEPONMUNICATION INFORMATION:

TELEPAN: (206) 622-4900

TELEPAN: (206) 622-4900

TELEPAN: (206) 622-631

INFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:
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Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia APPLICANT: Houghton, Raymond;
APPLICANT: Wedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
               ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 391; Conservative
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US-09-056-556-107
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US-09-072-596-102
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 391;
                                                                                                                                                                                                                             COUNTY: USA
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOEDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DSYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: USACITION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                             NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.8%; Score 1949; DB 4; I
100.0%; Pred. No. 9.4e-140;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/ACENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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STREET: 6300 Columbia Center, 701
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                             Sequence 111, Application US/08818112
Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
                                                                                                        Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
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Best Local Similarity 84.9%
Matches 337; Conservative
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                                                                                         GENERAL INFORMATION:
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US-08-818-112-111
            RESULT 10
US-08-818-112-111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 LIAINLIGQNIPAIAVNEAEYGEMWAQDAAAMFGYAAAIAIAILLPFEEAPEMTSAGG
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              APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.8%; Score 1949; DB 4; Length 391; Best Local Similarity 100.0%; Pred. No. 9.4e-140; Matches 391; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC_DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE: 05-MAY-1998
                                                                                                                                                                                                              E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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NAME: Maki, David J.
EEGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELBFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-4900
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                         Washington
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STRANDEDNESS: sir
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US-09-072-967-107
                                                                                                                                                                                                                                                                                                              98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                    CITY: Seattle STATE: Washing
                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SSAGLMVAAASPYVANMSVTAGQAELFAAQVRVAAAAYETAYGLTVPPVIAENRAELMI
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APPLICANT: Dillor, Davin C.
APPLICANT: Campos-Netc, Antonio
APPLICANT: Campos-Netc, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Caractaik, Daniel R.
TITLE OF INVENTION: COMPOUNDS NO TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 105/08/818,112 FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                             6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.0%; Score 1652.5; DB 3. 84.9%; Pred. No. 2.7e-117; iive 19; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION:
TELEDHONE: (206) 622-4900
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TREATME

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241 IVSMINNHVSMTNSGVSMASTLHSMLKGFAP-AAAQAVETAAQNGVQAMSSLGSQLGSSL 299
                                                                                       300 GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
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                                                           ĠSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG
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                                                                                                                                        365 GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                  360 GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David, U. 392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                        Sequence 111, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND MENUBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 396 amino acids TYPE: amino acid
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Best Local Similarity 84.9
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                              US-09-056-556-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 6
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300 GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIAINLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATALLPFEEAPEMTSAGG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 120
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                                                                                                                                                                                                                                                                                              Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Indels
                                                           360 GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
                                    365 GLPVGQMGARAG--GGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
BELICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                           3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1652.5; DB
Pred. No. 2.7e-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          Sequence 106, Application US/08818111
Patent No. 633852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                      Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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NAME: Maki, David J
REGISTRATION NUMBER: 21,392
REPERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION: INFORMATION:
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84.9%;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 396 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 84.9°
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COINUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
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STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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STREET: 63
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US-08-818-111-106
                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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249 MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAAVQTAAQNGVRAMSS----LGSSL 304
                                                                                                                                                                                                                                                         305 GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGOMLG 364
                                                                                                                                                                                                                                                                                      300 GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
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                                                                     189 ILLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                                                  APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Weddik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: HENDRICAND AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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55.0%; Score 1652.5; DB 4; Length 396;
Best Local Similarity 84.9%; Pred. No. 2.7e-117;
Matches 337; Conservative 19; Mismatches 34; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                              360 GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FTLING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 111, Application US/09072967
Patent No. 6592877
GENERAL INFORMATION:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 211
TELECOMMUNICATION: INFORMATION:
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INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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STREET: 6300 CO
CITY: Seattle
STATE: Washingt
COUNTRY: USA
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US-09-072-967-111
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US-09-072-967-111
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                                    305 GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VVDFGALPPEINSARMYAGPGSASLVAAAKKMDSVASDLFSAASAFQSVVWGLTTGSWIG 60
            MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAAQAVQTAAQNGVRAMSS----LGSSL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF INVENTION: 350
CORRESPONDENCE: 350
CORRESPONDENCE: COMPUSES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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COMPUTER: READABLE FORM:
MEDIUM TYPE: TIOPDY disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIPICATION:
                                                                                                                                                                                                                             365 GLPVGQMGARAG - GGLSGVLRVPPRPYVMPHSPAAG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6300 Columbia Center, 701 Fifth Avenue
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEFAK: (206) 622-6931
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              Sequence 106, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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Best Local Similarity 84.99
Matches 337; Conservative
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US-09-072-596-106
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SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI 128
                                                                                                                   LIATNILGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATILPFEEAPEMTSAGG 188
                                                                                                                                          LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
                                                                                                                                                                                                      MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSS----LGSSL 304
                                                                                                                                                                                                                                                                     241 IVSMIANNHVSMTNSGVSMASTIHSMIKGFAP-AAAQAVETAAQNGVQAMSSIGSQLGSSL 299
                                                                                                                                                                                                                                                                                                                                          300 GSSGLGAGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAQTAPGHMLG 359
                                                                                                                                                                                                                                                                                                                      GSSGLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLG 364
SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHODS FOR IMMUNOTHERAPY OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: TRM PC compatible
COBERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13 MAR-1997
ATTORNEY/APPLICATION: 424
ATTORNEY/APPLICATION:
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|GLPLGQLTNSGGGFGGVSNALRMPPRAYVMPRVPAAG 396
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 153
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Patent No. 6290969
GENERAL INFORMATION:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELEPOMMUNICATION INFORMATION:
TELEPAX: (206) 682-6900
TELEFAX: (206) 682-6911
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acide
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6300 Columbia Center,
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STATE: Washington
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ive 16; Mismatches 36;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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3007 1 HWHHHHHHWUDFGALPPEIN.....SGGPVVNGLGQVVGMNTAAS 596 BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-597-796C-10 Perfect score: Sequence: Scoring table:

Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Searched:

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB Maximum DB

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geneseqp1990s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

Mycobacterium tuberculosis antigen fusion protein Mtb59f. AAY32070 standard; protein; 596 AA. (first entry) 17-JAN-2000 AAY32070; AAY320

Tuberculosis, antigen, fusion protein, Mtbs9f, TbH9, Ra35, diagnosis, therapy, vaccine, immunogen. Location/Qualifiers Mycobacterium tuberculosis. Peptide

1. .8 /note= "Met/His tag" 9. .140 /note= "Ra12" 143. .596 /note= "TbH9" 99WO-US007717. 07-APR-1999; WO9951748-A2 14-OCT-1999. Protein Protein

98US-00056556. 98US-00223040. (CORI-) CORIXA CORP. 30-DEC-1998; 07-APR-1998;

Campos-Neto A; Skeiky YAW, Alderson M, WPI; 1999-601610/51. N-PSDB; AAZ20205. New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis. Claim 1; Fig 12A-B; 83pp; English.

This sequence represents a recombinant Mycobacterium tuberculosis bi-antigen Kusion protein, termed Mtb59f, composed of the antigens ThH9 and Ra35. The fusion protein is expressed in host cells using a vector carrying a polynucleotide (see AAZ20205) comprising the coding sequences

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for the 2 antigens. The invention provides fusion proteins (see AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M. tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein
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                                                                                                                                 standard; protein; 596
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(first entry)
                                                                                                                                                                                                        Vaccine; immunity; diag
MTB59F; fusion protein
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous conjugation polypeptide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a leishmania polymucleotide sequence encoding a polymucleotide sequence encoding a polymucleotide sequence encoding a polymucleotide sequence encoding a polymucleotide sequence encoding a polymucleotide sequence encoding a polympetide or its fragment. The Leishmania polymucleotide is selected from TSA, LeIF, MIS, and 64 polymucleotides of methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mycobacterium tuberculosis and TBH9 protein from Mycobacterium tuberculosis and TBH9 protein from Mycobacterium sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 98-99; 155pp; English
                                                                                                                                                                                                                                        <u>ب</u>
                                                                                                                                                                                                                                           Guderian
                                                                                                                                                    13-MAR-2001; 2001US-0275837P.
                                                                                                         13-MAR-2002; 2002WO-US008223
                                                                                                                                                                                                                                           Brannon M,
                                                                                                                                                                                                                                                                                       WPI; 2002-759844/82.
                                                                                                                                                                                              (CORI-) CORIXA CORP
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Mycobacterium sp. Mycobacterium tuberculosis. Chimeric.

29-AUG-2003 27-JAN-2003

AAE29710 AAE29710;

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Query Match 100.
Best Local Similarity 100.
Matches 596; Conservative
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08-MAY-2002
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          540
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                                                                                                                                                                                                                                                                                         Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a subject.
  PSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSG
                           QTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPG
                                      QTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPG
                                                    RVVALGOTVQASDSITGAEETINGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS 596
                                                                                                                                                   Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB59F; TbH9-Ra35 protein.
                                                              RVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS
                                                                                                                                       Mycobacterium species MTB59F fusion protein.
                                                                                                                                                                                                                                                                                                            5; Page 114-115; 136pp; English.
                                                                                                 AAE17574 standard; protein; 596 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TbH9-Ra35) fusion protein
                                                                                                                                                                                                                                                          Alderson M;
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01-FEB-2001; 2001US-0265737P
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                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                      WPI; 2002-147798/19
                                                                                                                                                                      Mycobacterium sp
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                                                                                                                                                           1 HMHHHHHHHWDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWG
                                                                                                                                                                                                                        LIVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIA
                                                                                                                                                                                                                                                                          61 LTVGSWIGSSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HMHHHHHHWVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWG
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                                                          Gaps
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/note= "OTHER= Xaa. Xaa= In frame stop codon"
     Length 596;
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tuberculostatic; immunogen; vaccine; Tb59-Ra35; Mtb59f.
                                                       Indels
100.0%; Score 3007; DB 5;
100.0%; Pred. No. 1.7e-198;
ive 0; Mismatches 0;
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polymucleotide sequence of Ra12, a 14 kba C-terminal fragment of serine protease antigen WTB32A of Mycobacterium tuberculosis, and a heterologous polymucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both cutaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another conlecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This sequence represents the Ra12-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142. MYDFGALPPEINSARMYAGPGSASLVAAAQMMDSVASDLFSAASAFQSVVWGLTVGSWIG 201
          QIYGVDVVGYDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
                                                                                                                                                                                                                                                                                                                                                          Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
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Best Local Similarity 100.0%; Pred. No. 3.4e-194;
Matches 588; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                  AAO22142 standard; protein; 729
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                                                                                                                                                                                                                                                                                                                                                                                                       immunogen; cytokine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents an M. tuberculosis fusion protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                         New fusion proteins of Mycobacterium tuberculosis antigens, useful diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis.
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                                                                                                                                                                                                                                           Dillon DC, Alderson M, Campos-Neto A;
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100.0%; Pred. No. 1.7e-198;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 12; 62pp; English
97US-00818112.
97US-00942578.
98US-00025197.
98US-00056556.
98US-00223040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 596; Conservative
                                                                                                                                                                                                       CAMPOS-NETO A.
                                                                                                                   REED S G.
SKEIKY Y A.
DILLON D C.
ALDERSON M.
                                                                                                                                                                                                                                           Skeiky YA,
                                                                                                                                                                                                                                                                                  WPI; 2002-171134/22.
N-PSDB; ABK14139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 599 AA;
                     01-OCT-1997;
18-FEB-1998;
07-APR-1998;
                                                                                   30-DEC-1998;
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB32A and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polynucelotide of the invention may have a use in gene therapy, and as a polynucelotide of the invention may have a use in gene therapy, and as a polynucelotide of the invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 308
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                                                                                                                                                                                                                                                                          142 MVDFGALPPBINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGGGGTPRAVPGRVVALGQT
                                                                                                                                                                                                                                                                                                                                    SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion protein, MTB32A, MTB39; antigen; MTB32A, MTB39, MTB85A, tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                           Length 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549 VQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS
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                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                       tch 98.0%; Score 2946; DB 7; L al Similarity 100.0%; Pred. No. 3.9e-194; 588; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
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Fig 15; 112pp; English.
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Mycobacterium sp.
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                                                                                                                  LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 248
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                                                                                                                                                                                                      MYSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG 441
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                                                                            LIATNLIGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATLLLPFEEAPEMTSAGG
                                                                                                                                         LIEGAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN
                                                                                                                                                                            MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                                                                                                                       LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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                 LIATNLLGONTPAIAVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGG
                                                                                                                                                                                                                                                                                              GOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV
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tuberculosis; tuberculostatic; gene therapy; vaccine.
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N-PSDB; ADA26360.
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Mycobacterium sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 875 AA;
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                                                                                                                                                                                                                      Mycobacterium
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                                                                                                                                                                          New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB93 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                                                                                                                                                                   85; Fig 14; 112pp; English.
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                                                                          15-FEB-2002; 2002US-0357351P.
                                                     18-FEB-2003; 2003WO-US004903
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 588; Conservative
                                                                                                                      Y, Guderian J,
                                                                                                                                          WPI; 2003-697554/66.
N-PSDB; ADA26359.
                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                              Sequence 825 AA;
        WO2003070187-A2
                             28-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid encoding a fusion polypeptide with the WTB32A and MTB39 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion protein, MTB32A, MTB39, antigen; MTB32A, MTB39, MTB85A, tuberculosis; tuberculostatic; gene therapy; vaccine.
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                               VQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS
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100.0%; Pred. No. 4.3e-194;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, or 6H polynucleotide, useful as vaccine to elicit protective immunity inst pathogenic microorganisms e.g. Leishmania and Mycobacterium
LLEQAAAVEEASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f) fusion protein.
                                                                                                                                                                                                     GOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSODRFADFPALPLDPSAMVAOV
                                                                               MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                                             LGGGVAANIGRAASVGSLSVPQAMAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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                                        MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                                                                                        LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGOMLGGLPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic agent; gene therapy; MTB72F; MAPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 129-132; 155pp; English.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-759844/82.
N-PSDB; AAD47110.
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Chimeric.
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27-JAN-2003
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are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microcoganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is Mycobacterium sp. MYP2.F-Leishmania sp. thiol specific antioxidant [TSA, MAPS (aka.r95f)] fusion protein. This sequence comprises Mycobacterium species MYP2.F (a 72 kDa poly-protein fusion construct comprising Ralz-TBH9-Ra35) linked to the Leishmania TSA (MAPS). (Updated on 29-AUG-2003) to standardise OS field)
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The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB35 antigen from a Mycobacterium species of the tuberculosts complex. A polypeptide of the invention has tuberculostatic activity. A polypeptide of the invention may have a use in gene therapy, and as a polymucelotide of the invention may have a use in gene therapy, and as a polymore. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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GYDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQT
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                                                                                                                                                                                                                                                                                                                                              fusion protein; MTB32A, MTB39; antigen; MTB32A, MTB39; MTB85A, tuberculosis; tuberculostatic; gene therapy; vaccine; MTB72F; 85B.
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                                                                bovis MTB72F and 85b complex antigen (fusion MTB103F).
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100.0%; Pred. No. 5.1e-194;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB33 antigens, with or without the MTB85A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 12; 112pp; English.
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N-PSDB; ADA26357.
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es 588; Conser
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                                           WO2003070187-A2
    Mycobacterium
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                                                                                                                                                          GPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVV 488
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 GOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDPSAMVAQV
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                                MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                            LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                             LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
                                                                                                                                                                                                    GYDRIQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVALGQT
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                                                                                                                   GOMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSODRFADFPALPLDPSAMVAQV
                                                                                                                                                                                                                                                                                                                                                                                                        fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
tuberculosis; tuberculostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                VOASDSLIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNIAAS 729
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                                                                                                                                                                                                                                                                                                                      protein; 1022
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                                                                                                                                                                                                                                                                                                                      standard;
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                                    Length 1022;
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tuberculosis; tuberculostatic; gene therapy; vaccine.
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                                      Score 2946; DB 7; I
Pred. No. 5.2e-194;
                        98.0%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                       Conservative
                                         Query Match
Best Local Similarity
Matches 588; Conserv
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Sequence 1022 AA;
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Mycobacterium sp. MTB72FMutSA fusion protein

(first entry)

29-AUG-2003 27-JAN-2003

AAE29709;

13-MAR-2002; 2002WO-US008223 13-MAR-2001; 2001US-0275837P

40200272792-A2.

Chimeric

19-SEP-2002

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(CORI-) CORIXA CORP

2002-759844/82.

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Vaccine; immunity; diagnostic agent; gene therapy; TbH9; antigen;
Ra35MutSA; Ra12; MTB72MutSA; fusion protein.
                                                                                                                                Mycobacterium sp.
Mycobacterium tuberculosis.
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                                                                                                                                                                The invention relates to a novel nucleic acid encoding a fusion polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and MTB85A antigen from a Mycobacterium species of the tuberculosis complex. A polypeptide of the invention has tuberculostatic activity. A polymucelotide of the invention may have a use in gene therapy, and as a polymucelotide of the invention may have a use in gene therapy, and as a posting in the major treating tuberculosis infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                   68
                                                                                New isolated nucleic acid encoding a fusion polypeptide with the MTB32A and MTB39 antigens, with or without the MTB35A antigen, from a Mycobacterium species, useful for diagnosing, preventing and/or treating tuberculosis infection.
                                                                                                                                                                                                                                                                                                                                                   MVDFGALPPEINSARMYAGPGSASLVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIG
                                                                                                                                                                                                                                                                                                                                                                 SSAGLMVAAASPYVAWMSVTAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMI
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100.0%; Pred. No. 6e-194;
live 0; Mismatches 0
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                      Guderian J,
                                               2003-697554/66.
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combinant nucleic acid molecule comprising a Leishmania TSA, LeIF, 6H polynucleotide, useful as vaccine to elicit protective immunity bathogenic microorganisms e.g. Leishmania and Mycobacterium
                                                                                                                                                                                                        The invention relates to a recombinant nucleic acid molecule encoding a pulsation polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected are used in MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                          microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polymucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is MTB72F fusion protein. This fusion protein comprises Ra35Mut5A mutant protein and Ra12 protein from M. tuberculosis and TbH9 protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)
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Pred. No. 5.4e-194;
1; Mismatches 0;
                                                                                                                                                     Disclosure; Page 93-95; 155pp; English
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LLEQAAAVEEASDTAAANQLMMNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISN 381
                                    MVSMANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSSG
                                                          GQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPALPLDDFSAMVAQV
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                                                                                                             LGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB72FMutSA; Ra12-TDH9-Ra35MutSA;
                                                                                                                                                                                                                                                                                                                                                                                                                          VQASDSLIGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTAAS 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium species MTB72FMutSA fusion protein.
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/label= Ra12_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky Y, Reed S, Alderson M;
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535. .729
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N-PSDB; AAD28343.
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the strological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and prevention of Mycobacterium infection. The diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymorlectides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or call-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A furstradermal skin test. The present sequence is Mycobacterium species mTB72FMutSA (Ral2-TbH9-Ra35MutSA) mutant fusion protein
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99.8%; Pred. No. 5.4e-194;
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Search completed: June 30, 2004, 16:48:49 Job time: 63.2853 secs